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CC -----
DR EMBL: U09269; AAB9457.1; -
DR EMBL: U74683; AAB58400.3; -
DR HSSP: O46427; 8PCH.
DR MEROPS: C01.070; -.
DR MGD: MGI:109553; Clsc.
DR InterPro: IPR000668; Peptidase_C1.
DR InterPro: IPR000169; Thiolprot_act_site.
DR Pfam: PF00112; Peptidase_C1; 1.
DR PRINTS: PR00705; PAPA1N.
DR PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
DR PROSITE: PS00640; THIOL_PROTEASE_ASN; 1.
KW Hydrolyase; Thiol protease; Lysosome; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 24
FT PROPEP 25 230
FT CHAIN 231 393
FT CHAIN 394 462
FT ACT_SITE 257 257
FT ACT_SITE 404 404
FT ACT_SITE 426 426
FT CARBOHYD 29 29
FT CARBOHYD 53 53
FT CARBOHYD 275 275
SQ SEQUENCE 462 AA; 52376 MW; 56574B8BD7DF4710 CRC64;

Query Match 7.1%; Score 89; DB 1; Length 462;
Best Local Similarity 23.6%; Pred. No. 1.1;
Matches 35; Conservative 19; Mismatches 52; Indels 42; Gaps 7;

OY 56 ACPELCEDEPCEPCISIVRYMLANFALANDNGCNCNPPLKHFDAEPFLQIA---- 111
DB 319 SCPEFYTAKDSF--CKPRENCLRYSSDYVVGFGCGCNALMKLELVKRPAAVAFEVH 376
OY 112 ----QYAGIVPAVAFRVPCEKGGGIRFTINGNDY--FDLVLTNNGAGDIRAVSLKGS 165
DB 377 DDFLHYHSGI-----YHHTGLSDPFNFEL---TN-----HAVLLGVG 411
OY 166 KTD-----QWOSMRNGMNGMNSNTYLR 188
DB 412 GRDPVTCIEWIIKNSGMSWGESGYFR 439

RESULT 11
GUN_MYTED STANDARD: PRT; 181 AA.
AC P82186;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
DE (CMCAsE).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE-Digestive gland;
RX MEDLINE=20389517; PubMed=10931178;
RA Xu B., Hellman U., Ersson B., Janson J.-C.;
RT Purification, characterization and amino-acid sequence analysis of a
RT thermolabile, low molecular mass endo-beta-1,4-glucanase from blue
RL Eur. J. Biochem. 267:4970-4977(1999).

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CC -----
CC - FUNCTION: ACTIVE TOWARDS THE SOLUBLE CARBOXYMETHYLCELLULOSE (CMC).
CC POSSESSES EXPANSIN ACTIVITY TOO.
CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.
CC - TISSUE SPECIFICITY: DIGESTIVE GLAND.
CC - MASS SPECTROMETRY: MW=19702; METHOD=MALDI.
CC - MISCELLANEOUS: Has an isoelectric point of 7.6. Its optimum pH is
CC 4.6 and optimum temperature is between 30-50 degrees Celsius.
CC - SIMILARITY: BELONGS TO CELLULOSE FAMILY K (FAMILY 45 OF GLYCOSYL
CC HYDROLASES).
DR InterPro: IPR000334; Glyco_hydro_45.
DR PROSITE: PS01140; GLYCOSYL_HYDROL_F45; FALSE_NEG.
KW Cellulose degradation; Hydrolase; Glycosidase.
FT ACT_SITE 24 24
FT ACT_SITE 132 132
FT DISULFID 4 16
FT DISULFID 30 69
FT DISULFID 32 176
FT DISULFID 65 178
FT DISULFID 72 157
FT DISULFID 103 113
SQ SEQUENCE 181 AA; 19711 MW; E00A8C57203823F6 CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 181;
Best Local Similarity 25.2%; Pred. No. 0.52;
Matches 36; Conservative 9; Mismatches 43; Indels 55; Gaps 7;

OY 8 GHATFYGADASGTWG-----GACGYGNLHSGY-----GLDTAALSTALPNSGCK---- 53
DB 6 GNPRRYNGSCASTYVYHDSHKACCGCPASGDAQCGMNAAGSVVAASQMYDSDGKKGWC 65
OY 54 ----CGACFELT-----CED---DPEWCTPGSIIVRYNLA 81
DB 66 GCHCGGCIKLTTGGYVPGCGPRVREGLSKTEWITNLCPIVYPNDMCMGSGQYGGHNKY 125
OY 82 NFALAND--NG-----GMCNP 95
DB 126 GYELHLDLENGRSQVYGMGMNPN 148

RESULT 12
MPL2_LOLPR STANDARD: PRT; 97 AA.
ID MPL2_LOLPR
AC P14947;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Pollen allergen Lol p 2-A (Lol p II-A).
DE Pollen perenne (Perennial ryegrass).
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Poace; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP SEQUENCE.
RX MEDLINE=89291864; PubMed=2472390;
RA Ansari A.A., Shenbagamurthi P., Marsh D.G.;
RT "Complete amino acid sequence of a Lolium perenne (perennial rye
RT grass) pollen allergen, Lol p II."
RL J. Biol. Chem. 264:11181-11185(1989).
CC - SUBCELLULAR LOCATION: Secreted.
CC - DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC - SIMILARITY: BELONGS TO THE LOI P I FAMILY OF ALLERGENS.
CC - SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
DR PIR: A34291; A34291.
DR HSSP: P43214; IWHO.
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR ProDom: PD002179; Pollen_allergen; 1.
DR PROSITE: PS00843; EXPANSIN_CBD; 1.
KW Allergen; Multigene family.
FT DOMAIN 15 96
FT VARIANT 29 29 S->A.

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ID CATC_HUMAN STANDARD: PRT: 463 AA.
AC P53634;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dipeptidyl-peptidase I precursor (EC 3.4.14.1) (DPP-I) (DPP1)
DE (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase).
GN CTSK OR CPPI
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN (1)
RN SEQUENCE FROM N.A.
RC TISSUE=ileum;
RX MEDLINE=95377428; PubMed=7649281;
RA Paris A., Struckel B., Pungertar J., Renko M., Dolenc I., Turk V.;
RT "Molecular cloning and sequence analysis of human preprocathepsin C";
RL FEBS Lett. 369:326-330(1995).
RN (2)
RN SEQUENCE FROM N.A.
RX MEDLINE=97248590; PubMed=9092576;
RA Rao N.V., Rao G.V., Hoidal J.R.;
RT "Human dipeptidyl-peptidase I. Gene characterization, localization,
RT and expression";
RL J. Biol. Chem. 272:10260-10265(1997).
RN (3)
RN VARIANTS PLS F-249; L-252; P-272; S-301; C-339 AND C-347.
RX MEDLINE=20047769; PubMed=10581027;
RA Toomes C., James J., Wood A.J., Wu C.L., McCormick D., Lench N.,
RA Hewitt C., Moynihan L., Roberts E., Woods C.G., Markham A., Wong M.,
RA Widmer R., Gaffar K.A., Pemberton M., Hussein I.R., Temtamy S.A.,
RA Davies R., Read A.P., Sloan P., Dixon M.J., Thakker N.S.;
RT "Loss-of-function mutations in the cathepsin C gene result in
RT peridontal disease and palmar/plantar keratosis";
RL Nat. Genet. 23:421-424(1999).
RN (4)
RN FUNCTION: THIOL PROTEASE. HAS DIPEPTIDYLPEPTIDASE ACTIVITY. CAN
RN DEGRADATE GLUCAGON.
RN (5)
RN CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Xbb-|-
RN xcc, except when xaa is Arg or Lys, or xbb or xcc is Pro.
RN (6)
RN COFACTOR: REQUIRES CHLORIDE IONS FOR ACTIVITY.
RN (7)
RN SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN CROSS-LINKED
RN BY A DISULFIDE BOND.
RN (8)
RN SUBCELLULAR LOCATION: Lysosomal.
RN (9)
RN DISEASE: DEFECTS IN CTSK ARE A CAUSE OF PAPILLON-LEFEVRE SYNDROME
RN (PLS) ALSO KNOWN AS KERATOSIS PALMOPLANTARIS WITH
RN PERIODONTOPATHIA. IT IS AN AUTOSOMAL RECESSIVE DISORDER THAT IS
RN MAINLY ASCERTAINED BY DENTISTS BECAUSE OF THE SEVERE PERIODONTITIS
RN THAT AFFECTS PATIENTS. BOTH THE DECIDUOUS AND PERMANENT
RN DENTITIONS ARE AFFECTED, RESULTING IN PREMATURE TOOTH LOSS.
RN PALMOPLANTAR KERATOSIS, VARYING FROM MILD PSORIASIFORM SCALY SKIN
RN TO OVERT HYPERKERATOSIS, TYPICALLY DEVELOPS WITHIN THE FIRST THREE
RN YEARS OF LIFE. KERATOSIS ALSO AFFECTS OTHER SITES SUCH AS ELBOWS
RN AND KNEES.
RN (10)
RN SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
RN PAPAN FAMILY OF THIOL PROTEASES.
RN (11)
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RN between the Swiss Institute of Bioinformatics and the EMBL outstation -
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RN entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
RN or send an email to license@isb-sib.ch).
RN (12)
RN EMBL: X87212; CA60671.1; -;
RN EMBL: U79415; AAC51341.1; -;
RN HSSP: O46427; 8PCH.
RN MEROPS: C01.070; -;
RN MIM: 602365; -;
RN MIM: 245000; -;
RN InterPro: IPR000668; Peptidase_C1.
RN InterPro: IPR000169; thiolprol_act_site.

DR Pfam: PF00112; Peptidase_C1; 1.
DR PRINTS: PR00705; PAPAN.
DR PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
DR PROSITE: PS00640; THIOL_PROTEASE_ASN; 1.
DR Hydrolyse: Thiol protease; Lysosome; Glycoprotein; Zymogen; Signal;
KW Disease mutation.
FT SIGNAL 1 24
FT PROPEP 25 230
FT CHAIN 231 394
FT CHAIN 395 463
FT ACT_SITE 258 258
FT ACT_SITE 405 405
FT ACT_SITE 427 427
FT CARBOHYD 29 29
FT CARBOHYD 53 53
FT CARBOHYD 119 119
FT CARBOHYD 216 216
FT CARBOHYD 249 249
FT VARIANT 252 252
FT VARIANT 272 272
FT VARIANT 301 301
FT VARIANT 339 339
FT VARIANT 347 347
FT VARIANT 347 347
FT VARIANT 51841 MM; 51841 MM; 759BSEF1290C3771 CRC64;
SQ SEQUENCE 463 AA; 51841 MM; 759BSEF1290C3771 CRC64;
Query Match 6.7%; Score 83; DB 1; Length 463;
Best Local Similarity 25.3%; Pred. No. 3.6;
Matches 37; Conservative 9; Mismatches 62; Indels 38; Gaps 6;
QY 56 ACFELTCDDEPKIPSIIVRYNLANFALANDNGMCNPRLKHFDAEPALQIA---- 111
DB 320 ACFPYTGDSF--CKMKEDCFRYSSEHYVSGFYGGCNEALMKLELVHNGPMAVFEVY 377
QY 112 ---QYRAGIVPAFRVRVPCCKGGIRFTINGNPYFDLVITVVGAGAGDIRAVSLKGSY 167
DB 378 DDFLHYKKGIYHNTGLRDPF-----NPF-----ELTN-----HALLVGYGT 414
QY 168 DQNGSM-----SRWQGNQMSNTLYLR 188
DB 415 DSASGMVYIVKXSWGCGENGCFR 440
RESULT 15
GN2_TRIRE STANDARD: PRT: 418 AA.
AC P07982;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Endoglucanase EG-II precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
DE (Cellulase).
GN BGL2 OR BGLII.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_Taxid=51453;
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN-VTT-D-80133;
RX MEDLINE=88255850; PubMed=3384334;
RA Saloheimo M., Lehtovaara P., Penttilae M., Teeri T.T., Staahlberg J.,
RA Johansson G., Pettersson G., Claysens M., Tonne P., Knowles J.K.C.;
RT "EgII, a new endoglucanase from Trichoderma reesei: The
RT characterization of both gene and enzyme";
RL Gene 63:11-21(1988).
RN (2)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:53:05 : Search time 11.2915 Seconds

(without alignments)
1914.721 Million cell updates/sec

Title: US-09-896-301-5

Perfect score: 1245

Sequence: 1 DNGCMERGHATFYGGADASG.....SYDVVPHDMQRCGFEEGGQF 225

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1203.5	96.7	255	2	T50656 expansin EXP2 [imp
2	962	77.3	250	2	T110079 expansin S1 precu
3	958.5	77.0	253	2	F84631 probable expansin
4	927	74.5	232	2	T09821 expansin (clone pp
5	927	74.5	232	2	T09826 expansin (clone pp
6	923	74.1	232	2	T09818 expansin (clone pp
7	912	73.3	232	2	T09825 expansin (clone pp
8	912	73.3	238	2	T09786 expansin - upland
9	884	71.0	246	2	T04175 expansin - rice
10	883	70.9	251	2	T03298 expansin 2 - rice
11	869	69.8	237	2	T50654 expansin EXP1 [imp
12	868	69.7	248	2	C84444 probable expansin
13	851	68.4	257	2	D84820 probable expansin
14	850	68.3	252	2	T02530 probable expansin
15	846	68.0	260	2	T47689 probable expansin
16	844	67.8	258	2	S53082 expansin-like prot
17	834	67.0	257	2	T50658 expansin 9 [import
18	833	66.9	257	2	T02727 expansin EXP6 [imp
19	832	66.8	259	2	T50653 expansin 18 - toma
20	832	66.8	255	2	T05573 expansin 1 - toma
21	828	66.5	261	2	T07630 alpha-expansin OSE
22	828	66.5	264	2	T50659 alpha-expansin OSE
23	825	66.3	258	2	T48247 alpha-expansin-like prot
24	819	65.8	260	2	T08016 alpha-expansin
25	819	65.8	262	2	T50660 probable expansin
26	814	65.4	258	2	T10083 alpha-expansin 2 [
27	809.5	65.0	255	2	T50655 expansin EXP5 [imp
28	761	61.1	255	2	T02010 expansin homolog T
29	759	61.0	252	2	F86335 hypothetical prote

30	758.5	60.9	261	2	T03737 expansin - rice
31	694.5	55.8	255	2	T03299 expansin 3 - rice
32	619	49.7	160	2	T09871 expansin - upland
33	609	48.9	257	2	G96654 hypothetical prote
34	602	48.4	257	2	F86259 protein T12C24.10
35	532	42.7	256	2	T05648 expansin homolog F
36	287	23.1	77	2	T09815 expansin (clone pp
37	278.5	22.4	262	2	S38620 allergen Phl p 1 -
38	272	21.8	102	2	T09828 allergen Phl p 1 -
39	272	21.8	263	2	T04301 beta-expansin - ri
40	266.5	21.4	491	2	F96681 beta-expansin [imp
41	266	21.4	261	2	T04301 beta-expansin [imp
42	261	21.0	277	2	S48032 beta-expansin [imp
43	259	20.8	259	2	T50657 beta-expansin [imp
44	259	20.8	271	2	H84592 beta-expansin [imp
45	257	20.6	263	2	S13614 major allergen Lol

ALIGNMENTS

RESULT 1

T50656 expansin EXP2 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000

C:Accession: T50656

R:Shcherban, T.Y.; Shi, J.; Durackho, D.M.; Gullitnan, M.J.; McQueen-Mason, S.J.; Shi

Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995

A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu

A:Reference number: Z14894, PMID:96016146

A:Accession: T50656

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-255 <SNC>

A:Cross-references: EMBL:U00481; PDB:AMB38073.1

A:Experimental source: variety Columbia

C:Genetics:

C:Gene: EXP2

C:Function:

A:Description: Induces extension (creep) in plant cell walls

C:Superfamily: expansin

C:Keywords: cell wall

Query Match

Best Local Similarity

Matches 220: Conservative

1; Mismatches 4; Indels 3; Gaps 1;

Score 1203.5; DB 2; Length 255; Pred. No. 9.1e-102;

1 DNGCMERGHATFYGGADASGTMGACGYGNLSHSGYGLQTPALSTALFNSGKCGACFEL 60

28 DNGCMERGHATFYGGADASGTMGACGYGNLSHSGYGLQTPALSTALFNSGKCGACFEL 87

61 TCDDDEKICPGSTIV---RYNLANFALANDNGCMNPLKFDLAEPFLQIAQYRACI 117

88 TCDDDEKICPGSTIV---RYNLANFALANDNGCMNPLKFDLAEPFLQIAQYRACI 117

118 VPAPEFRVPCCKGGRFTINCPYFDVLITNVGACGIRAVSLKSGSTDDWQSMNRW 177

148 VPAPEFRVPCCKGGRFTINCPYFDVLITNVGACGIRAVSLKSGSTDDWQSMNRW 207

178 GGNWQSNTRYLRGQSLFQVTDSDGRTVVSVDVPPHDMQRCGFEEGGQF 225

208 GGNWQSNTRYLRGQSLFQVTDSDGRTVVSVDVPPHDMQRCGFEEGGQF 255

RESULT 2

T10079 expansin S1 precursor - cucumber

C:Species: Cucumis sativus (cucumber)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T10079

R:Shcherban, T.Y.; Shi, J.; Durackho, D.M.; Gullitnan, M.J.; McQueen-Mason, S.J.; Shi

Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995

A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi
 A:Reference number: Z14894; MUID:96016146
 A:Accession: T10079
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-250 <SHC>
 A:Cross-references: EMBL:U30382; NID:g1040874; PIDN:AAB37746.1; PID:g1040875
 A:Experimental source: cultivar Burpee Pickler
 A:Genetics:
 A:Gene: EXP1
 C:Function:
 A:Description: mediates cell wall extension
 C:Superfamily: expansin
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-250/Product: expansin #status predicted <MAT>

Query Match 77.3%; Score 962; DB 2; Length 250;
 Best Local Similarity 75.0%; Pred. No. 7.4e-80;
 Matches 171; Conservative 26; Mismatches 27; Indels 4; Gaps 2;

QY 1 DNGGWHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGQKGCACFEL 60
 DB 24 DYGWQHATFYGGADAGTGMGACGYGNLYSGYGTNTVALSTALFNSGQKGCACFEM 83

QY 61 TCEDDEPWCIPGSIIVY--RYNLANFALANDNGMCNPLKHPDLAPAFLOIAQYRAGI 117
 DB 84 TCTNDPCKMCLPCTIRYATATNFCPPNFALPNNNGMCNPLDHPMAEPALQIAQYRAGI 143

QY 118 VVAFRRVPCERGGGIRFTINGNPFEDLVLTITNGAGADIRAVSLKSKTDQMSRMW 177
 DB 144 VVPSFRVPCMKKGGVRFITNGHSYFNVLITITNGAGADIVHSVLSKSRG--WQMSRMW 202

QY 178 GOMWOSNTYLKQSLSPGYTSDGRTVYSYDVYPHDMQFGOTFEGGOF 225
 DB 203 GOMWOSNTYLKQSLSPGYTSDGRTVLTAYNLVPSNMQFGOTFEGGOF 250

RESULT 3
 F84831
 probable expansin [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C:Accession: F84831
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKien, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: F84831
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-253 <STO>
 A:Cross-references: GB:AEO02093; NID:g2651297; PIDN:AAB87577.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g40610
 A:Map position: 2
 C:Superfamily: expansin

Query Match 77.0%; Score 958.5; DB 2; Length 253;
 Best Local Similarity 74.3%; Pred. No. 1.6e-79;
 Matches 171; Conservative 23; Mismatches 29; Indels 7; Gaps 2;

QY 1 DNGGWHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGQKGCACFEL 60
 DB 26 DYGWQHATFYGGADAGTGMGACGYGNLYSGYGTNTVALSTALFNSGQKGCACFEM 85

QY 61 TCEDDEPWCIPGSIIVY--RYNLANFALANDNGMCNPLKHPDLAPAFLOIAQYRAGI 115
 DB 86 KONDPRKCGSTITV--TATNFCPPNPGLSNDNGMCNPLDHPMAEPALQIAQYRAGI 143

QY 116 GIVPAFRVPCERGGGIRFTINGNPFEDLVLTITNGAGADIRAVSLKSKTDQMSRMW 175

DB 144 GIVPSFRVPCMKKGGVRFITNGHSYFNVLITITNGAGADIVHSVLSKSRG--WQMSRMW 203

QY 176 NWGOMWOSNTYLKQSLSPGYTSDGRTVYSYDVYPHDMQFGOTFEGGOF 225
 DB 204 NWGOMWOSNTYLKQSLSPGYTSDGRTVLTAYNLVPSNMQFGOTFEGGOF 253

RESULT 4
 T09821
 expansin (clone ptxp3) - loblolly pine (fragment)
 C:Species: Pinus taeda (loblolly pine)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
 C:Accession: T09821
 R:Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
 submitted to the EMBL Data Library, July 1996
 A:Description: Expansins are conserved in conifers and expressed in response to exoge
 A:Reference number: Z16866
 A:Accession: T09821
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-232 <HUT>
 A:Cross-references: EMBL:U64891; NID:g1778100; PID:g1778101
 A:Experimental source: clone ptxp3
 C:Superfamily: expansin

Query Match 74.5%; Score 927; DB 2; Length 232;
 Best Local Similarity 72.9%; Pred. No. 1e-76;
 Matches 164; Conservative 26; Mismatches 31; Indels 4; Gaps 2;

QY 3 GGMERGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGQKGCACFEL 62
 DB 8 GGMERGHATFYGGADAGTGMGACGYGNLYSGYGTNTVALSTALFNSGQKGCACFEM 83

QY 63 EDDPWCIPGSIIVY--RYNLANFALANDNGMCNPLKHPDLAPAFLOIAQYRAGI 119
 DB 68 NDDPWCIPGSIIVY--RYNLANFALANDNGMCNPLKHPDLAPAFLOIAQYRAGI 127

QY 120 VAFRRVPCERGGGIRFTINGNPFEDLVLTITNGAGADIRAVSLKSKTDQMSRMW 179
 DB 128 ILYTRVPCIRKGGIRFTINGNPFEDLVLTITNGAGADIVHSVLSKSRG--WQMSRMW 202

QY 180 NMOSNTYLKQSLSPGYTSDGRTVYSYDVYPHDMQFGOTFEGGOF 224
 DB 187 NMOSNTYLKQSLSPGYTSDGRTVLTAYNLVPSNMQFGOTFEGGOF 251

RESULT 5
 T09826
 expansin (clone ptxp5) - loblolly pine (fragment)
 C:Species: Pinus taeda (loblolly pine)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
 C:Accession: T09826
 R:Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
 submitted to the EMBL Data Library, July 1996
 A:Description: Expansins are conserved in conifers and expressed in response to exoge
 A:Reference number: Z16866
 A:Accession: T09826
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-232 <HUT>
 A:Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105
 A:Experimental source: clone ptxp5
 C:Superfamily: expansin

Query Match 74.5%; Score 927; DB 2; Length 232;
 Best Local Similarity 72.9%; Pred. No. 1e-76;
 Matches 164; Conservative 26; Mismatches 31; Indels 4; Gaps 2;

QY 3 GGMERGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGQKGCACFEL 62
 DB 8 GGMERGHATFYGGADAGTGMGACGYGNLYSGYGTNTVALSTALFNSGQKGCACFEM 83

QY 63 EDDPWCIPGSIIVY--RYNLANFALANDNGMCNPLKHPDLAPAFLOIAQYRAGI 119

A:Residues: 1-246 <CHO>
 A:Cross-references: EMBL:U85246; NID:g1815680; PIDN:AAB81662.1; PID:g1815681
 A:Experimental source: cv. Pin Gaew 56
 C:Genetics:
 A:Gene: EXP4
 C:Superfamily: expansin

Query Match 71.0%; Score 884; DB 2; Length 246;
 Best Local Similarity 71.2%; Pred. No. 8.7e-73;
 Matches 161; Conservative 23; Mismatches 38; Indels 4; Gaps 2;

QY 3 GGMERGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGOKGACFELTC 62
 DB 22 GGMOSAHATFYGGADAGTGMGACGYGNLSQYGTNTAALSTALFNDGACGSCFELTC 81
 QY 63 EDDPEWCIPGSIIV--RYNLANFALANDNGWCNPLKHPDLAPAFLOIAOYRAGIYP 119
 DB 82 DNAGSSCLPGSIVTATNFCPPNYGLPSDDGWCNPPRPHFDMAPAFLOIAOYRAGIYP 141
 QY 120 VAFRRVPCERKGGIRFTINGNPFEDLVLTITNVGAGDIRAVSLKSKTDQMSRNMGQ 179
 DB 142 VSRRRVPCVARKGGIRFTVNSHSYFNLTITNVAGADVRSVSIKSRGTG-WQPMNRMGQ 200
 QY 180 NMOSNTYLRGOSLSFQYTDSDGRVVSVDYVPHDMQFGOTFEFGGF 225
 DB 201 NMOSNATLDGOSLSFQYTDSDGRVVSNNVAHPGMOFGOTFEFGGF 246

RESULT 10

T03298
 C:Species: Oryza sativa (rice)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
 C:Accession: T03298
 R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shieh,
 Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
 A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi
 A:Reference number: 214894; MUID:96016146
 A:Accession: T03298
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-251 <SHC>
 A:Cross-references: EMBL:U30477; NID:g1041709; PIDN:AAB38074.1; PID:g1041710
 C:Genetics:
 A:Gene: EXP2
 C:Function:
 A:Description: induces extension (creep) in plant cell
 C:Superfamily: expansin

Query Match 70.9%; Score 883; DB 2; Length 251;
 Best Local Similarity 70.2%; Pred. No. 1.1e-72;
 Matches 160; Conservative 24; Mismatches 40; Indels 4; Gaps 3;

QY 1 DNGMERGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGOKGACFELTC 60
 DB 25 DYGSMOSAHATFYGGADAGTGMGACGYGNLSTGYGTNTAALSTALFNDGACGSCFELTC 84
 QY 61 TCEDPEWCIPGSI-IVRYNLAA--NFALANDNGWCNPLKHPDLAPAFLOIAOYRAGI 117
 DB 85 RCDNDGOMCLPGSVTATNLCPPNYALPNDGWCNPPRPHFDMAPAFLOIGYRAGI 144
 QY 118 VPAFRVPCERKGGIRFTINGNPFEDLVLTITNVGAGDIRAVSLKSKTDQMSRNMGQ 177
 DB 145 VPAFRVPCVARKGGIRFTINGHSYFNLTITNVAGADVRSVSIKSRGTG-WQPMNRMGQ 203
 QY 178 GOMOSNTYLRGOSLSFQYTDSDGRVVSVDYVPHDMQFGOTFEFGGF 225
 DB 204 GOMOSNTYLRGOSLSFQYTDSDGRVVSNNVAHPGMOFGOTFEFGGF 251

RESULT 11
 T50654
 expansin EXP1 [imported] - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
 C:Accession: T50654
 R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shi
 Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
 A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
 A:Reference number: 214894; MUID:96016146
 A:Accession: T50654
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-237 <SHC>
 A:Cross-references: EMBL:U30476; PIDN:AAB38070.1
 C:Genetics:
 A:Gene: EXP1
 C:Function:
 A:Description: induces extension (creep) in plant cell walls
 C:Superfamily: expansin
 C:Keywords: cell wall

Query Match 69.8%; Score 869; DB 2; Length 237;
 Best Local Similarity 69.3%; Pred. No. 1.9e-71;
 Matches 156; Conservative 28; Mismatches 37; Indels 4; Gaps 2;

QY 3 GGMERGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGOKGACFELTC 62
 DB 12 GGMVNAHATFYGGADAGTGMGACGYGNLSQYGTNTAALSTALFNDGACGSCFELTC 71
 QY 63 EDDPEWCIPGSIIV--RYNLANFALANDNGWCNPLKHPDLAPAFLOIAOYRAGIYP 119
 DB 72 QNDGKWCCLPGSIVTATNFCPPNYGLPSDDGWCNPPRPHFDMAPAFLOIAOYRAGIYP 131
 QY 120 VAFRRVPCERKGGIRFTINGNPFEDLVLTITNVGAGDIRAVSLKSKTDQMSRNMGQ 179
 DB 132 VAFRRVPCVARKGGIRFTINGHSYFNLTITNVAGADVRSVSIKSRGTG-WQPMNRMGQ 190
 QY 180 NMOSNTYLRGOSLSFQYTDSDGRVVSVDYVPHDMQFGOTFEFGGF 224
 DB 191 NMOSNTYLRGOSLSFQYTDSDGRVVSNNVAHPGMOFGOTFEFGGF 235

RESULT 12

C84444
 probable expansin [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C:Accession: C84444
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Unayam, L.; Tallon,
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: C84444
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-248 <STO>
 A:Cross-references: GB:AE002093; NID:g3461833; PIDN:AC32927.1; GSPDB:GND0139
 C:Genetics:
 A:Gene: At2g03090
 A:Map position: 2
 C:Superfamily: expansin

Query Match 69.7%; Score 868; DB 2; Length 248;
 Best Local Similarity 67.8%; Pred. No. 2.5e-71;
 Matches 154; Conservative 31; Mismatches 38; Indels 4; Gaps 2;

QY 2 NGMERGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGOKGACFELTC 61
 DB 22 DAGVNAHATFYGGADAGTGMGACGYGNLSQYGTNTAALSTALFNDGACGSCFELTC 81
 QY 62 CEDPEWCIPGSIIV--RYNLANFALANDNGWCNPLKHPDLAPAFLOIAOYRAGIYP 118
 DB 82 CQSDGAWCLPGLATVATNFCPPNYALPNDGWCNPPRPHFDMAPAFLOIGYRAGIYP 141

Sun Oct 13 14:19:05 2002

us-09-896-301-5.rpr

||||| | ||||| || | : : | : ||||| |
Db 211 GQNMOSNAVLVGOGLSFRTVTSDDRTSTSMNIAPSNMOPGOTFGKNE 258

Search completed: October 11, 2002, 15:01:00
Job time : 11.2915 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:54:05 ; Search time 8.80074 Seconds
(without alignments)
624,466 Million cell updates/sec

Title: US-09-896-301-5

Perfect score: 1245

Sequence: 1 DNGGWERGHATFYGGADASG.....SYDVVPHDMQFGQFFEGGQF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1245	100.0	225	2	US-08-440-517A-5
2	1245	100.0	225	4	US-09-092-160-5
3	962	77.3	227	4	US-09-092-160-7
4	863.5	69.4	226	2	US-08-440-517A-6
5	863.5	69.4	226	4	US-09-092-160-6
6	859	69.0	228	2	US-08-440-517A-2
7	859	69.0	228	4	US-09-092-160-2
8	777.5	62.4	222	2	US-08-440-517A-3
9	777.5	62.4	222	4	US-09-092-160-3
10	734	59.0	225	4	US-09-362-642-2
11	732	58.8	225	2	US-08-845-539-2
12	685.5	55.1	179	2	US-08-845-539-6
13	685.5	55.1	179	4	US-09-362-642-6
14	660.5	53.1	227	2	US-08-440-517A-4
15	660.5	53.1	227	4	US-09-092-160-4
16	609	48.9	167	2	US-08-845-539-4
17	609	48.9	167	4	US-09-362-642-4
18	277	22.2	261	1	US-07-971-096-2
19	277	22.2	261	1	US-08-175-096-2
20	257.5	20.7	246	4	US-08-441-507-21
21	257	20.6	263	1	US-07-971-096-4
22	257	20.6	263	1	US-08-175-096-4
23	257	20.6	263	4	US-08-413-974-6
24	257	20.6	263	4	US-08-434-418-6
25	257	20.6	263	4	US-08-433-288-6
26	257	20.6	263	4	US-08-174-739A-6
27	256.5	20.6	272	4	US-08-441-507-15

28	236.5	19.0	245	4	US-08-441-507-24	Sequence 1, Appl
29	204	16.4	200	4	US-08-441-507-4	Sequence 4, Appl
30	203	16.3	197	4	US-08-441-507-5	Sequence 5, Appl
31	152	12.2	145	4	US-08-413-974-4	Sequence 4, Appl
32	152	12.2	145	4	US-08-434-418-4	Sequence 4, Appl
33	152	12.2	145	4	US-08-433-288-4	Sequence 4, Appl
34	152	12.2	145	4	US-08-174-739A-4	Sequence 4, Appl
35	142	11.2	145	4	US-08-441-507-2	Sequence 2, Appl
36	140	11.2	145	4	US-08-441-507-16	Sequence 16, Appl
37	135	10.8	138	4	US-08-441-507-7	Sequence 7, Appl
38	129.5	10.4	122	4	US-08-441-507-23	Sequence 23, Appl
39	107.5	8.6	54	3	US-08-750-419A-12	Sequence 12, Appl
40	97.5	7.8	86	4	US-08-441-507-8	Sequence 8, Appl
41	85.5	6.9	1147	1	US-08-144-121-3	Sequence 3, Appl
42	85.5	6.9	1147	2	US-08-735-893-3	Sequence 3, Appl
43	85.5	6.9	1165	1	US-08-144-121-2	Sequence 2, Appl
44	85.5	6.9	1165	2	US-08-735-893-2	Sequence 2, Appl
45	83	6.7	463	1	US-08-426-428-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-08-440-517A-5
; Sequence 5, Application US/08440517A
; Patent No. 5959082
; GENERAL INFORMATION:
; APPLICANT: COSGROVE, DANIEL J.;
; APPLICANT: GUILTINAN, MARK;
; APPLICANT: SCHERBAN, TATYANA;
; APPLICANT: SHI, JUN
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
; ADDRESS: PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,517A
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
; US-08-440-517A-5
;
; Query Match 100.0%; Score 1245; DB 2; Length 225;
; Best local similarity 100.0%; Pred. No. 3, 6e-128;
; Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 DNGGWERGHATFYGGADASGTMGACGYNLHSGYGLQTAALSTALFNSGCKGACPEL 60
Db 1 DNGGWERGHATFYGGADASGTMGACGYNLHSGYGLQTAALSTALFNSGCKGACPEL 60
Qy 61 TCEDDPENCIGSITIVRYNLANPALANDNGWCNBPPLKHFDLAPAFLOIAQYRAGIVPV 120
Db 61 TCEDDPENCIGSITIVRYNLANPALANDNGWCNBPPLKHFDLAPAFLOIAQYRAGIVPV 120
Qy 121 AFRVPCKKGGGIRFTTNGNPFYDLVLTNNYGAGDIPRAVSLKSKTDQWQMSRNNQCN 180
Db 121 AFRVPCKKGGGIRFTTNGNPFYDLVLTNNYGAGDIPRAVSLKSKTDQWQMSRNNQCN 180
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QY 181 WOSNTYLRGOSLSFOYTDSDGRTVSYDVVPHDMQFGQTEGGOF 225
DB 181 WOSNTYLRGOSLSFOYTDSDGRTVSYDVVPHDMQFGQTEGGOF 225

RESULT 2

US-09-092-160-5
; Sequence 5, Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Gullitnan, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/092,160C
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 08/440,517
; EARLIER FILING DATE: 1995-05-12
; EARLIER APPLICATION NUMBER: 08/242,090
; EARLIER FILING DATE: 1994-05-12
; EARLIER APPLICATION NUMBER: 08/060,944
; EARLIER FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
; OTHER INFORMATION: expansin
US-09-092-160-5

Query Match 100.0%; Score 1245; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.6e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DNGWGERGHATFFYGADASGTMGACGYGNLHSGYGLQTAALSTALFNSGKGCACFEL 60
DB 1 DNGWGERGHATFFYGADASGTMGACGYGNLHSGYGLQTAALSTALFNSGKGCACFEL 60
QY 61 TCEDDPEMCIPGSIIVRYNLANFALNDGWCNPLKHFDLAEPALQIAQYRAGI 120
DB 61 TCEDDPEMCIPGSIIVRYNLANFALNDGWCNPLKHFDLAEPALQIAQYRAGI 120
QY 121 AFFRVPCERKGGIRFTINGNPFEDLVLTNNVGAGADIRAVSLKSKTKDQMSRMNGN 180
DB 121 AFFRVPCERKGGIRFTINGNPFEDLVLTNNVGAGADIRAVSLKSKTKDQMSRMNGN 180
QY 181 WOSNTYLRGOSLSFOYTDSDGRTVSYDVVPHDMQFGQTEGGOF 225
DB 181 WOSNTYLRGOSLSFOYTDSDGRTVSYDVVPHDMQFGQTEGGOF 225

RESULT 3

US-09-092-160-7
; Sequence 7, Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Gullitnan, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/092,160C
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 08/440,517

EARLIER FILING DATE: 1995-05-12
; EARLIER APPLICATION NUMBER: 08/242,090
; EARLIER FILING DATE: 1994-05-12
; EARLIER APPLICATION NUMBER: 08/060,944
; EARLIER FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cucumber
; OTHER INFORMATION: expansin
US-09-092-160-7

Query Match 77.3%; Score 962; DB 4; Length 227;
Best Local Similarity 75.0%; Pred. No. 3e-97;
Matches 171; Conservative 26; Mismatches 27; Indels 4; Gaps 2;

QY 1 DNGWGERGHATFFYGADASGTMGACGYGNLHSGYGLQTAALSTALFNSGKGCACFEL 60
DB 1 DNGWGERGHATFFYGADASGTMGACGYGNLHSGYGLQTAALSTALFNSGKGCACFEL 60
QY 61 TCEDDPEMCIPGSIIV--RYNLANFALNDGWCNPLKHFDLAEPALQIAQYRAGI 117
DB 61 TCEDDPEMCIPGSIIVRYNLANFALNDGWCNPLKHFDLAEPALQIAQYRAGI 120
QY 118 VVPAFRVPCERKGGIRFTINGNPFEDLVLTNNVGAGADIRAVSLKSKTKDQMSRMNGN 177
DB 121 VVPAFRVPCERKGGIRFTINGNPFEDLVLTNNVGAGADIRAVSLKSKTKDQMSRMNGN 179
QY 178 GONWOSNTYLRGOSLSFOYTDSDGRTVSYDVVPHDMQFGQTEGGOF 225
DB 180 GONWOSNTYLRGOSLSFOYTDSDGRTVSYDVVPHDMQFGQTEGGOF 227

RESULT 4

US-08-440-517A-6
; Sequence 6, Application US/08440517A
; Patent No. 5959082
; GENERAL INFORMATION:
; APPLICANT: COSGROVE, DANIEL J.;
; APPLICANT: GULLITNAN, MARK;
; APPLICANT: SCHERBAN, TATYANA;
; APPLICANT: SHI, JUN
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
; ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,517A
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
US-08-440-517A-6

Query Match 69.4%; Score 863.5; DB 2; Length 226;

Best Local Similarity 69.3%; Pred. No. 1.7e-86;
Matches 158; Conservative 24; Mismatches 41; Indels 5; Gaps 4;

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OY 1 DNGMGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGKCGACFEL 60
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Db 1 DYSWOSAHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGKCGACFEL 59
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 61 TCEDDEPMICPGSI-IVRYNLA--NFALANDNGMCNPLKHFDAEPALQIAYRAGI 117
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 RCNDNGOMCLPGSVYVATNLCPPNYALPNDGCGMCNPPRPFDAEPALQIAYRAGI 119
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 118 VVAARVPCVCEKGGIRFTINGNPNFYDLVLTNNVGAGDIRAVSLKSKTDQMSMRNW 177
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Db 120 VVAVSYRRVPCVCKGIRFTINGHSYFNLVLTNNVAGPCGVOSVSIKGSSTG-WQPMRNM 178
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 178 GGNMOSNTYLRGQSLSFQVYTSDDGRTVVSIDVVPDHMOFGQTFEGGOF 225
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 179 GGNMOSNTYLRGQSLSFQVAVNSDGRITVSNVYPAGWQFGQTFEGGOF 226
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 5
US-09-092-160-6

```

: Sequence 6, Application US/09092160C
: Patent No. 6255466
: GENERAL INFORMATION:
: APPLICANT: Cosgrove, Daniel J
: APPLICANT: McQueen-Mason, Simon
: APPLICANT: Guiltinan, Mark J
: APPLICANT: Sheridan, Tatyana
: APPLICANT: Shi, Jun
: TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
: FILE REFERENCE: 1194/1C114053
: CURRENT APPLICATION NUMBER: US/09/092,160C
: EARLIER FILING DATE: 1998-06-05
: EARLIER APPLICATION NUMBER: 08/440,517
: EARLIER FILING DATE: 1995-05-12
: EARLIER APPLICATION NUMBER: 08/242,090
: EARLIER FILING DATE: 1994-05-12
: EARLIER APPLICATION NUMBER: 08/060,944
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent Ver. 2.1
: SEQ ID NO 6
: LENGTH: 226
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
: OTHER INFORMATION: expansin
US-09-092-160-6

```

Query Match 69.4%; Score 863.5; DB 4; Length 226;
Best Local Similarity 69.3%; Pred. No. 1.7e-86;
Matches 158; Conservative 24; Mismatches 41; Indels 5; Gaps 4;

```

OY 1 DNGMGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGKCGACFEL 60
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DYSWOSAHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGKCGACFEL 59
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 61 TCEDDEPMICPGSI-IVRYNLA--NFALANDNGMCNPLKHFDAEPALQIAYRAGI 117
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 RCNDNGOMCLPGSVYVATNLCPPNYALPNDGCGMCNPPRPFDAEPALQIAYRAGI 119
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 118 VVAARVPCVCEKGGIRFTINGNPNFYDLVLTNNVGAGDIRAVSLKSKTDQMSMRNW 177
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120 VVAVSYRRVPCVCKGIRFTINGHSYFNLVLTNNVAGPCGVOSVSIKGSSTG-WQPMRNM 178
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 178 GGNMOSNTYLRGQSLSFQVYTSDDGRTVVSIDVVPDHMOFGQTFEGGOF 225
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 179 GGNMOSNTYLRGQSLSFQVAVNSDGRITVSNVYPAGWQFGQTFEGGOF 226
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 6

US-08-440-517A-2

```

: Sequence 2, Application US/08440517A
: Patent No. 5959082
: GENERAL INFORMATION:
: APPLICANT: COSGROVE, DANIEL J.;
: APPLICANT: GUITTINAN, MARK;
: APPLICANT: SHERIDAN, TATYANA;
: APPLICANT: SHI, JUN
: TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
: ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
: STREET: 113 TECHNOLOGY CENTER
: CITY: UNIVERSITY PARK
: STATE: PENNSYLVANIA
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 16802-7000
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK
: COMPUTER: NEC 286
: OPERATING SYSTEM: DOS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/440,517A
: FILING DATE:
: CLASSIFICATION: 530
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 228
: TYPE: AMINO ACID
: TOPOLOGY: UNKNOWN
US-08-440-517A-2

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Query Match 69.0%; Score 859; DB 2; Length 228;
Best Local Similarity 69.1%; Pred. No. 5.3e-86;
Matches 154; Conservative 28; Mismatches 37; Indels 4; Gaps 2;

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OY 3 GGNMGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGKCGACFEL 62
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Db 3 GGNMGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGKCGACFEL 62
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 63 EDDPEMPCISIV--RNLANFALANDNGMCNPLKHFDAEPALQIAYRAGI 119
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 QNDGKMCIPGSIYVATNLCPPNYALPNDGCGMCNPPRPFDAEPALQIAYRAGI 122
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 120 VAVRVPCEKGGIRFTINGNPNFYDLVLTNNVGAGDIRAVSLKSKTDQMSMRNW 179
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 123 VAVRVPCEKGGIRFTINGHSYFNLVLTNNVAGPCGVOSVSIKGSSTG-WQPMRNM 181
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 180 NMOSONTYLRGQSLSFQVYTSDDGRTVVSIDVVPDHMOFGQTFEGGOF 222
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 182 NMOSONTYLRGQSLSFQVAVNSDGRITVSNVYPAGWQFGQTFEGGOF 224
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 7
US-09-092-160-2

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: Sequence 2, Application US/09092160C
: Patent No. 6255466
: GENERAL INFORMATION:
: APPLICANT: Cosgrove, Daniel J
: APPLICANT: McQueen-Mason, Simon
: APPLICANT: Guiltinan, Mark J
: APPLICANT: Sheridan, Tatyana
: APPLICANT: Shi, Jun
: TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
: FILE REFERENCE: 1194/1C114053
: CURRENT APPLICATION NUMBER: US/09/092,160C
: EARLIER FILING DATE: 1998-06-05
: EARLIER APPLICATION NUMBER: 08/440,517
: EARLIER FILING DATE: 1995-05-12
: EARLIER APPLICATION NUMBER: 08/242,090
: EARLIER FILING DATE: 1994-05-12

```

```

1  EARLIER APPLICATION NUMBER: 08/060,944
2  EARLIER FILING DATE: 1993-05-12
3  NUMBER OF SEQ ID NOS: 7
4  SOFTWARE: PatentIn Ver. 2.1
5  SEQ ID NO 2
6  LENGTH: 228
7  TYPE: PRT
8  ORGANISM: Artificial Sequence
9  FEATURE:
10 OTHER INFORMATION: Description of Artificial Sequence: rice expansin
11 FEATURE:
12 NAME/KEY: UNSURE
13 LOCATION: 211
14 OTHER INFORMATION: Xaa is unknown or other.
15 US-09-092-160-2

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QY 3 GGMERGHATFFYGGADASTGTMGACGYGMLHSOQYGIOTAAISTLTFNMSGKCGACGFFLTG 62

Db 3 GGMVAHAHTFFYGGGASSTGMSGACGYGMLYSQGYGTNATSLTFLNNGLSGACGFFIRC 62

QY 63 EDDPEMCIFGSIIV--RYNLANFALANDNGMCNPPLKHPDLAEPAFLQIAQYRAQIVP 119

Db 63 QMDGKWCIFGSIIVYATATNFCPPNPANLPPNAGMGWCPNPQHPHDLSQLPFAORIAQYRAQIVP 122

QY 120 VAFRRVPCPEGGGIIFETTINGNPFEDVLTITVGGAGDIRAVSLKGSKTDDQMSRRNGQ 179

Db 123 VAYRRVPCVRRRGIFETTINGHSYFNLVITVGGAGDVHSAAMVKGSRGT-
WQAMSRRNGQ 18

QY 180 NMOSMTYLRGOSLSPQYIMDDSGRTVSYDVYVHDMQFQOTPEG 222

Db 182 NMOSNLYLRGOSLSERKVTTSDDQITVSNXNNAAGNSPQOTFTG 224

RESULT 8
 US-08-440-517A-3
 ; Sequence 3, Application US/08440517A
 ; Patent No. 5959082
 ; GENERAL INFORMATION:
 ; APPLICANT: COSGROVE, DANIEL J.;
 ; APPLICANT: GULLITMAN, MARK;
 ; APPLICANT: SHCHERBAN, TATYANA;
 ; APPLICANT: SHI, JUN
 ; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
 ; ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
 ; STREET: 113 TECHNOLOGY CENTER
 ; CITY: UNIVERSITY PARK
 ; STATE: PENNSYLVANIA
 ; COUNTRY: UNITED STATES OF AMERICA
 ; ZIP: 16802-7000
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: NEC 286
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/440,517A
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 222
 ; TYPE: AMINO ACID
 ; TOPOLOGY: UNKNOWN
 ;
 ; US-08-440-517A-3
 ;
 ; Query=Match
 ;
 ; 62.48% Score 777.5; DB 2; Length 222;

[illegible]

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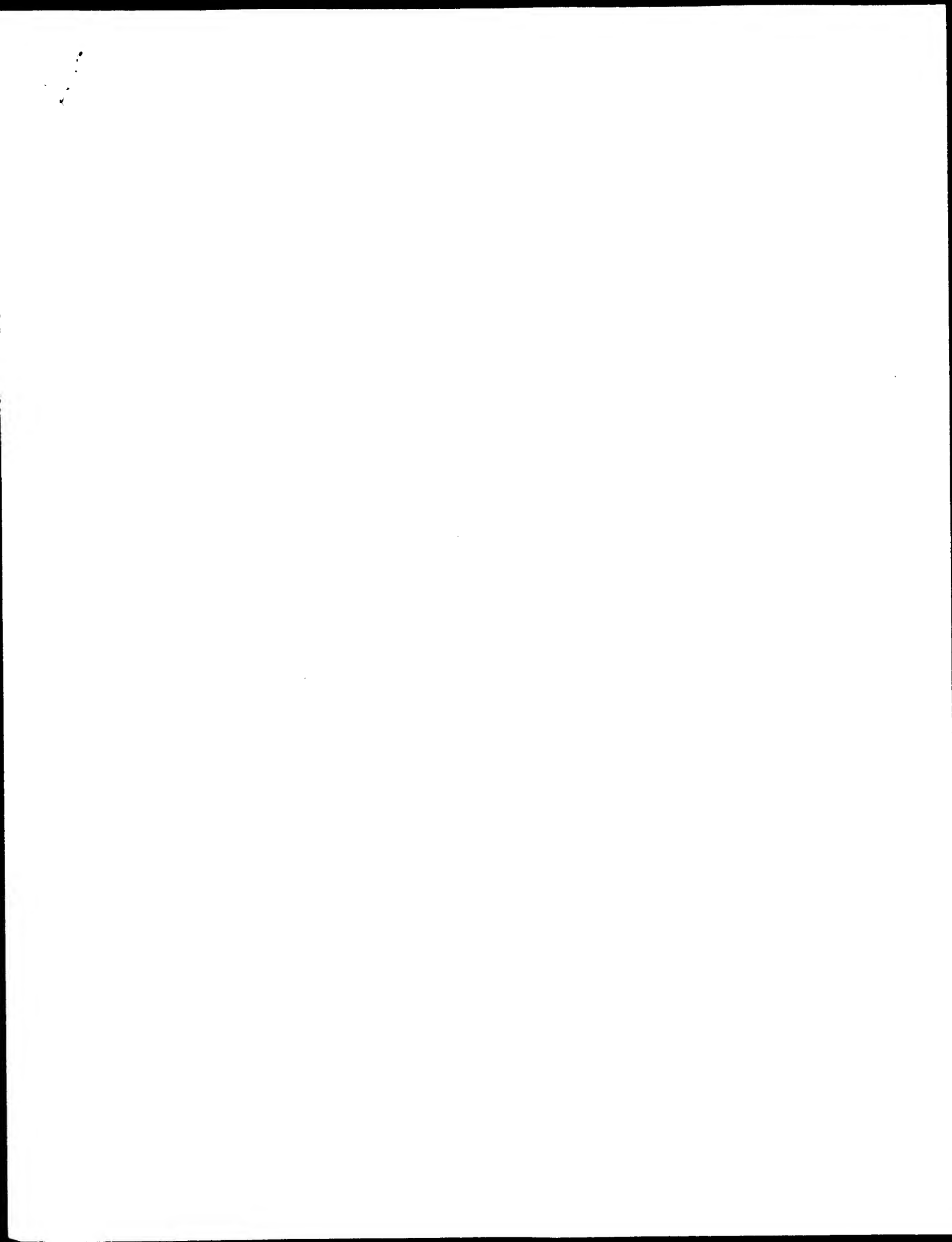
RESULT 9
US-09-092-160-3
; Sequence 3: Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Gullthnan, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/7C1140S3
; CURRENT APPLICATION NUMBER: US/09/092,160C
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 08/440,517
; EARLIER FILING DATE: 1995-05-12
; EARLIER APPLICATION NUMBER: 08/242,090
; EARLIER FILING DATE: 1994-05-12
; EARLIER APPLICATION NUMBER: 08/060,944
; EARLIER FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: rice expansin
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (14)..(58)
; OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160-3

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[illegible]

Query Match	53.1%	Score 660.5;	DB 4;	Length 227;
Best Local Similarity	57.8%	Pred. NO. 2.5e-64;		
Matches 122;	Conservative 33;	Mismatches 49;	Indels 7;	Gaps 4;

Search completed: October 11, 2002, 15:02:07
Job time : 9.80074 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:49:55 : Search time 24.9077 Seconds
(without alignments)
1003.367 Million cell updates/sec

Title: US-09-896-301-5

Perfect score: 1245

Sequence: 1 DNGGWERGHATFYGGADASG.....SYDVVPHDWQFGQTFEGGQF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1245	100.0	225	17	AA94531
2	962	77.3	227	17	AA94527
3	958.5	77.0	253	21	AA94543
4	958.5	77.0	253	21	AA94543
5	912	73.3	241	21	AA60546
6	912	73.3	241	21	AA60546
7	912	73.3	241	21	AA60547
8	912	73.3	249	21	AA60545
9	912	73.3	249	21	AA60545
10	912	73.3	249	21	AA60546
11	912	73.3	259	21	AA60544

12	912	73.3	259	21	AA651631	Arabidopsis thaliana
13	912	73.3	280	21	AA651645	Arabidopsis thaliana
14	868	69.7	251	21	AA638852	Arabidopsis thaliana
15	868	69.7	251	21	AA643343	Arabidopsis thaliana
16	868	69.7	253	21	AA638851	Arabidopsis thaliana
17	868	69.7	253	21	AA643342	Arabidopsis thaliana
18	868	69.7	281	21	AA643341	Arabidopsis thaliana
19	868	69.7	282	21	AA638850	Arabidopsis thaliana
20	859	69.0	228	17	AA645528	Rice expansin. Or
21	858	68.9	242	21	AA636570	Arabidopsis thaliana
22	858	68.9	249	21	AA636569	Arabidopsis thaliana
23	858	68.9	255	21	AA636568	Arabidopsis thaliana
24	856.5	68.8	207	21	AA625444	Arabidopsis thaliana
25	856.5	68.8	207	21	AA646484	Arabidopsis thaliana
26	853	68.5	227	17	AA645332	Arabidopsis thaliana
27	853	68.5	241	21	AA605453	Arabidopsis thaliana
28	853	68.5	249	21	AA605452	Arabidopsis thaliana
29	853	68.5	255	21	AA605451	Arabidopsis thaliana
30	851	68.4	257	21	AA636445	Arabidopsis thaliana
31	850	68.3	262	21	AA629931	Arabidopsis thaliana
32	850	68.3	273	21	AA629930	Arabidopsis thaliana
33	843	67.7	250	22	AA600414	Tomato seed expans
34	833	66.9	255	21	AA630325	Arabidopsis thaliana
35	833	66.9	257	21	AA630324	Arabidopsis thaliana
36	825	66.3	250	21	AA609622	Arabidopsis thaliana
37	825	66.3	258	21	AA609621	Arabidopsis thaliana
38	825	66.3	280	21	AA609620	Arabidopsis thaliana
39	814	65.4	263	22	AA600412	Tomato seed expans
40	809.5	65.0	221	21	AA615694	Arabidopsis thaliana
41	809.5	65.0	221	21	AA651013	Arabidopsis thaliana
42	809.5	65.0	255	21	AA615693	Arabidopsis thaliana
43	809.5	65.0	255	21	AA651012	Arabidopsis thaliana
44	777.5	62.4	222	17	AA645529	Rice expansin. Or
45	765	61.4	210	21	AA629932	Arabidopsis thaliana

ALIGNMENTS

RESULT 1
AA94531
ID AA94531 standard; Protein: 225 AA.
XX
AC AA94531:
XX
XX 08-JUL-1996 (first entry)
DT
XX Arabidopsis expansin.
DE Arabidopsis expansin.
XX
XX Expansin: plant cell wall; cellulose; paper recycling; de-linking;
KW polysaccharide.
XX
XX Arabidopsis sp.
OS
XX
XX AU9540262-A.
PN
XX
XX 04-APR-1996.
PD
XX
XX 12-MAY-1994; 94AU-0068320.
PF
XX
XX 12-MAY-1995; 95US-0440517.
PR
XX 12-MAY-1993; 93US-0060944.
XX
XX (PENN-) PENN STATE RES FOUND.
PA
XX Cosgrove DJ, McQueen-Mason S;
XX WPI: 1996-201150/21.
DR
XX
XX Expansin proteins which alter the mechanical strength of
PT poly:saccharide(s) - useful in paper mfr. and recycling
XX
PS Disclosure: Page 32; 60pp; English.

XX Expansins are a novel class of proteins that catalyse the extension
CC of plant cell walls and the weakening of the hydrogen bonds in pure
CC cellulose. 2 expansins (AAR94528 and AAR94529) have been identified in
CC rice and 3 in Arabidopsis (AAR94530-32). A cDNA clone (AAT13320)
CC coding for cucumber expansin 29 (AAR94527) has been obtd. Expansins
CC can be used e.g. in the mfr., de-inking and recycling of paper, in
CC the textile industry, to aid delignification processes, to alter gel
CC mechanical strength, etc.

XX Sequence 225 AA;

Query Match 100.0%; Score 1245; DB 17; Length 225;
Best Local Similarity 100.0%; Pred. No. 4,7e-124;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DNGWEGHATFFYGADASTGAGCGYGNLHSGYGLQTAALSTALFNSGKGCACFEL 60
DB 1 DNGWEGHATFFYGADASTGAGCGYGNLHSGYGLQTAALSTALFNSGKGCACFEL 60
QY 61 TCEDDEPWCIPGSIIVRYNLANFALANDNGWCNPLKHFDAEPALQIAQYRAGI 120
DB 61 TCEDDEPWCIPGSIIVRYNLANFALANDNGWCNPLKHFDAEPALQIAQYRAGI 120
QY 121 AFRVPECEKGGIRFTINGNPFYDLVLTINVGAGDIRAVSLKSKTDQMSRMNGN 180
DB 121 AFRVPECEKGGIRFTINGNPFYDLVLTINVGAGDIRAVSLKSKTDQMSRMNGN 180
QY 181 WQNTYLRGQSLSFQYTDSDGRIVSYDVYPHDMQFGQTEGGQF 225
DB 181 WQNTYLRGQSLSFQYTDSDGRIVSYDVYPHDMQFGQTEGGQF 225

RESULT 2

AAR94527 standard; Protein; 227 AA.

XX AAR94527;

DT 08-JUL-1996 (first entry)

XX Cucumber expansin-29.

KW Expansin-29; plant cell wall; cellulose; paper recycling; de-inking;
KM polysaccharide; cucumber.

OS Cucumis sativus var. Burpee Pickler.

PN A09540262-A.

PD 04-APR-1996.

PF 12-MAY-1994; 94AU-0068330.

PR 12-MAY-1995; 95US-0440517.

PR 12-MAY-1995; 93US-0060944.

PA (PENN-) PENN STATE RES FOUND.

PI Cosgrove DJ, McQueen-Mason S;

DR WPI; 1996-201150/21.

DR N-PSDB; AAT13320.

XX Expansin proteins which alter the mechanical strength of
PT poly:saccharide(s) - useful in paper mfr. and recycling
XX Claim 7; Page 30; 60pp; English.

CC Cucumber expansin-29 (AAR94527) is a member of a novel class of
CC proteins that catalyse the extension of plant cell walls and the
CC weakening of the hydrogen bonds in pure cellulose. It can be obtd.
CC by expression of an isolated cDNA clone (see AAT13320) in bacterial or

CC other host cells. Expansin proteins have also been identified in oat
CC coleoptiles, in Arabidopsis (see AAR94530-32) and in rice (AAR94528-29),
CC and appear to be broadly distributed throughout the plant kingdom.
CC Expansins can be used e.g. in the mfr., de-inking and recycling of
CC paper, in the textile industry, to aid delignification processes, to
CC alter gel mechanical strength, etc.

XX Sequence 227 AA;

Query Match 77.3%; Score 962; DB 17; Length 227;
Best Local Similarity 75.0%; Pred. No. 5,9e-94;
Matches 171; Conservative 26; Mismatches 27; Indels 4; Gaps 2;

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DB 1 DNGWEGHATFFYGADASTGAGCGYGNLHSGYGLQTAALSTALFNSGKGCACFEL 60
QY 61 TCEDDEPWCIPGSIIV--RYNLANFALANDNGWCNPLKHFDAEPALQIAQYRAGI 117
DB 61 TCEDDEPWCIPGSIIVRYNLANFALANDNGWCNPLKHFDAEPALQIAQYRAGI 120
QY 118 VYAFRRVPECEKGGIRFTINGNPFYDLVLTINVGAGDIRAVSLKSKTDQMSRMNG 177
DB 121 VYAFRRVPECEKGGIRFTINGNPFYDLVLTINVGAGDIRAVSLKSKTDQMSRMNG 179
QY 178 GQNMQNTYLRGQSLSFQYTDSDGRIVSYDVYPHDMQFGQTEGGQF 225
DB 180 GQNMQNTYLRGQSLSFQYTDSDGRIVSYDVYPHDMQFGQTEGGQF 227

RESULT 3

AAG25443 standard; Protein; 253 AA.

XX AAG25443;

DI 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 29510.

KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 200DEP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
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RESULT 6
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DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 65551.

KW Protein identification: signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
KM	termination sequence.			
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Query Match 73.3%; Score 912; DB 21; Length 241;
Best Local Similarity 71.2%; Pred. No. 1.3e-88;
Matches 161; Conservative 30; Mismatches 31; Indels 4; Gaps 2;

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AC AAG06545;
DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 3356.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

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Query Match 73.3%; Score 912; DB 21; Length 249;
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RESULT 9
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DE Arabidopsis thaliana protein fragment seq ID NO: 65550.
 DE Protein identification: signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

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OS		PR 30-JUN-1999;	990S-0141287.
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QY	63 EDDPEWICPGSITV--RYNLANFLANDNGMCNPRLKHFDLAEPFLQIAYRAGIVP	119			
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QY	120 VAFRRVPCEKGCGIRFTINGNPEDVLITLTNGGAGDTRAVSLGSKTDQMGRMMGO	179			
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QY	180 NMOSNTYLRCQSLSFQVTDSDGRTVSYDYVPDHMQFGQTEEGEQF	225			
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DT	18-OCT-2000 (first entry)				

DE	Arabidopsis thaliana protein fragment SPO ID NO: 65569.
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KM	Protein identification: signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter,
XX	termination sequence.
OS	Arabidopsis thaliana.
XX	
PN	EPI033405-A2.
PD	
XX	06-SEP-2000.
PF	
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XX DT
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XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX PN EPI033405-A2.
XX PD 06-SEP-2000.
XX PE 25-FEB-2000; 2000EP-0301439.
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PR 28-OCT-1999; 990S-0161920.
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PR 28-OCT-1999; 990S-0161993.
PR 29-OCT-1999; 990S-0162142.

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Query Match 73.3%; Score 912; DB 21; Length 259;
 Best Local Similarity 71.2%; Pred. No. 1,5e-88;
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QY 63 EDDMWCIPGSIIV--RYNLANPALNDNGMGNPPLKHFLEPAFLQIAOYRACIIV 119
DB 94 ENDGKWCIPGSIIVTATNFCPPNNAALNNGMGNPPLKHFLEPAFLQIAOYRACIIV 153
QY 120 VAFRRVPECKGGIRFTTNGPNPYDLVLTINVGAGADIRAVSLGKSTDOMQSRWMO 179
DB 154 VSYRVRPCRRRGIRFTTNGHSYFLVLTINVGAGADIVHSAIKGSRF-VWQAMSRWMO 212
QY 180 NMQSTYTLRGOSLSHQVYDSGGRVVSVDVPHMOEGGEGEGGOF 225
DB 213 NMQSNSTYTLRGOSLSHQVYDSGGRVVSVDVPHMOEGGEGGOF 258

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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PN EPI03405-A2.
XX
PD 06-SEP-2000.
XX
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 73.3%; Score 912; DB 21; Length 280;
Best Local Similarity 71.2%; Pred. No. 1,6e-88;

Matches 161; Conservative 30; Mismatches 31; Indels 4; Gaps 2;

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OY 63 EDDPEMCIGESTIV---RYNLANFALANDNGCMCNPLKHFDLAPPAFLQIAQYRAGIVP 119

DB 115 ENDGKNCLEPSISIVATINCPNNALANNNGMCNPLEHFDLAPVQRIAQYRAGIVP 174
OY 120 VAFRRVPCERKGGIRFTINGNPFEDLYLTNNVGAGADIRAVLSKSKTDQMSRNMGQ 179
Db 175 VSTRRVPCRRRGICIRFTINGSHFNLVLTNNVGAGADIVSAIKSRP-VWQAMSRRMGQ 233
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AC AAC23852;
XX 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 27311.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
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Query Match 69.7%; Score 868; DB 21; Length 251;
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Db 85 QSDGAMCRLGALIVATNFCPPNALFNNAAGGCMNPLHFLDPSVFORIAQIACIV 14
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Db 145 PVSYRRPFCMRGGIRFTTNGHSYFNLLVLTNMGAGDVHSAVKSRIR-RDQMSRRNG 20
OY 179 QNNQNTIYLRGQSLDFQYDSDGRFRVSYDYVDHPDQFQGTFFGCGGF 225
Db 204 QNNQNNLLNCGALSKFTYADSGRTVVSNNIAPLSMWSFEGTFFGGRGF 250

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DT 18-OCT-2000 (first entry)
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terminations; termination sequence.

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Search completed: October 11, 2002, 14:56:43
 Job time : 25.9077 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:51:00 : Search time 19.5144 Seconds
(without alignments)
2003.488 Million cell updates/sec

Title: US-09-896-301-6
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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3: sp_bacteria:*
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17: sp_archaeap:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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25	969.5	77.1	237	10	038863
26	969.5	77.1	237	10	038863
27	964.5	76.7	240	10	094636
28	963.5	76.7	220	10	094636
29	960.5	76.4	249	10	094636
30	951.5	75.7	249	10	094636
31	948	75.4	253	10	094636
32	942.5	75.0	252	10	094636
33	938.5	74.7	248	10	080622
34	938.5	74.7	263	10	092932
35	937	74.5	249	10	094636
36	937	74.5	253	10	094636
37	935.5	74.4	250	10	094636
38	932.5	74.2	276	10	094636
39	923.5	73.5	259	10	094636
40	922	73.3	259	10	094636
41	919	73.1	255	10	094636
42	917	73.0	255	10	094636
43	916	72.9	242	10	094636
44	912.5	72.6	249	10	094636
45	910.5	72.4	264	10	094636

ALIGNMENTS

RESULT 1
ID 040636 PRELIMINARY: PRT: 251 AA.

AC 040636: 01-NOV-1996 (TREMURBL_01, Created)
DT 01-NOV-1996 (TREMURBL_01, Last sequence update)
DT 01-DEC-2001 (TREMURBL_19, Last annotation update)
DE EXPANSIN OS-EXP2.
GN OS-EXP2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPPONBARE;
RX MEDLINE=96016146; PubMed=7568110;
RA Sheehan T.Y., Shi J., Duracko D.M., Gullitman M.J.,
"Molecular cloning and sequence analysis of expansins--a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RT Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RL EMBL: U30477; AAB38074.1;
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSIN_FAM1.
DR PRODOM: PD002179; Pollen_allergen; 1.
SQ SEQUENCE 251 AA: 2969GCD57B454286 CRC64;

Query Match 97.9%; Score 1230.5; DB 10; Length 251;
Best Local Similarity 98.2%; Pred. No. 2.2e-103;
Matches 223; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 DYSSWQSAHATFGGDSAGTGCNLYSTGY-TNPAALSTVLPNDACRSCEYL 59
DB 25 DYSSWQSAHATFGGDSAGTGCNLYSTGY-TNPAALSTVLPNDACRSCEYL 84

QY 60 RCDNDGOMCLPGSVTATNLCPPNYALPNDGGMCPNPPRPFHMAEPALQIGYRAGI 119
 DB 85 RCDNDGOMCLPGSVTATNLCPPNYALPNDGGMCPNPPRPFHMAEPALQIGYRAGI 144
 QY 120 VPSYRRVPCVKKGIRFTINGHSYFNLVLTNVAAGDVQSVISGSSGTGMPMSRNWG 179
 DB 145 VPSYRRVPCVKKGIRFTINGHSYFNLVLTNVAAGDVQSVISGSSGTGMPMSRNWG 204
 QY 180 QNMOSNSYLDGOSLSFOVAASDGRVTYSNNVVPAGMOFGOTFEFGGF 226
 DB 205 QNMOSNSYLDGOSLSFOVAASDGRVTYSNNVVPAGMOFGOTFEFGGF 251

RESULT 2

Q9461 PRELIMINARY; PRT; 251 AA.
 AC Q9461;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE ALPHA-EXPANSIN.
 GN EXP2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriharididae; Oryzaeae; Oryza.
 RX NCBL_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21521099; PubMed=11641069;
 RA Lee Y., Choi D., Kende H.;
 RT *Expansins: ever-expanding numbers and functions.*;
 RL Curr. Opin. Plant Biol. 4:527-532(2001).
 DR EMBL: AF394544; AAL24480.1; -
 SQ SEQUENCE 251 AA; 26674 MW; C45036570EFE3BD CRC64;

Query Match 97.9%; Score 1230.5; DB 10; Length 251;
 Best local similarity 98.2%; Pred. No. 2.2e-103;
 Matches 223; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DYSSWOSAHATFFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 59
 DB 25 DYSSWOSAHATFFYGGDASGTMGTCGYGNLYSTGYTNTAALSTVLFNDGAACRSCYEL 84
 QY 60 RCDNDGOMCLPGSVTATNLCPPNYALPNDGGMCPNPPRPFHMAEPALQIGYRAGI 119
 DB 85 RCDNDGOMCLPGSVTATNLCPPNYALPNDGGMCPNPPRPFHMAEPALQIGYRAGI 144
 QY 120 VPSYRRVPCVKKGIRFTINGHSYFNLVLTNVAAGDVQSVISGSSGTGMPMSRNWG 179
 DB 145 VPSYRRVPCVKKGIRFTINGHSYFNLVLTNVAAGDVQSVISGSSGTGMPMSRNWG 204
 QY 180 QNMOSNSYLDGOSLSFOVAASDGRVTYSNNVVPAGMOFGOTFEFGGF 226
 DB 205 QNMOSNSYLDGOSLSFOVAASDGRVTYSNNVVPAGMOFGOTFEFGGF 251

RESULT 3

Q94KT7 PRELIMINARY; PRT; 253 AA.
 AC Q94KT7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE ALPHA-EXPANSIN PRECURSOR.
 GN EXP1.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoidae; Andropogoneae; Zea.
 RX NCBL_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21249159; PubMed=11351085;
 RA Wu Y., Mealey R.B., Cosgrove D.J.;
 RT "Analysis and Expression of the alpha-Expansin and beta-Expansin Gene
 Families in Maize.";
 RL Plant Physiol. 126:222-232(2001).
 DR EMBL: AF332169; AAK56119.1; -
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 1 20 POTENTIAL.
 253 AA; 26423 MW; 7CDD5390E0104099 CRC64;

Query Match 89.9%; Score 1130.5; DB 10; Length 253;
 Best local similarity 89.4%; Pred. No. 2.4e-94;
 Matches 203; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 1 DYSSWOSAHATFFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 59
 DB 27 DYSSWOSAHATFFYGGDASGTMGTCGYGNLYSTGYTNTAALSTVLFNDGAACRSCYEL 86
 QY 60 RCDNDGOMCLPGSVTATNLCPPNYALPNDGGMCPNPPRPFHMAEPALQIGYRAGI 119
 DB 87 RCDNDGOMCLPGSVTATNLCPPNYALPNDGGMCPNPPRPFHMAEPALQIGYRAGI 146
 QY 120 VPSYRRVPCVKKGIRFTINGHSYFNLVLTNVAAGDVQSVISGSSGTGMPMSRNWG 179
 DB 147 VPSYRRVPCVKKGIRFTINGHSYFNLVLTNVAAGDVQSVISGSSGTGMPMSRNWG 206
 QY 180 QNMOSNSYLDGOSLSFOVAASDGRVTYSNNVVPAGMOFGOTFEFGGF 226
 DB 207 QNMOSNSYLDGOSLSFOVAASDGRVTYSNNVVPAGMOFGOTFEFGGF 253

RESULT 4

P93442 PRELIMINARY; PRT; 246 AA.
 AC P93442;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE EXPANSIN.
 GN OS-EXP4.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriharididae; Oryzaeae; Oryza.
 RX NCBL_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PIN GAEM 56; TISSUE=INTERNODE;
 RX MEDLINE=97480100; PubMed=9338967;
 RA Cho H.T., Kende H.;
 RT *Expression of expansin genes is correlated with growth in deepwater
 rice.*;
 RL Plant Cell 9:1661-1671(1997).
 DR EMBL: 085246; AAB81662.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR PRODOM: PD002179; Pollen_allergen; 1.
 SQ SEQUENCE 246 AA; 25898 MW; CC01823A37BD084F CRC64;

Query Match 87.3%; Score 1097.5; DB 10; Length 246;
 Best local similarity 87.2%; Pred. No. 2.2e-91;
 Matches 197; Conservative 7; Mismatches 21; Indels 1; Gaps 1;

QY 2 YSSWOSAHATFFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 60
 DB 21 YSSWOSAHATFFYGGDASGTMGTCGYGNLYSTGYTNTAALSTVLFNDGAACRSCYEL 80
 QY 61 RCDNDGOMCLPGSVTATNLCPPNYALPNDGGMCPNPPRPFHMAEPALQIGYRAGI 120
 DB 81 RCDNDGOMCLPGSVTATNLCPPNYALPNDGGMCPNPPRPFHMAEPALQIGYRAGI 140
 QY 121 VPSYRRVPCVKKGIRFTINGHSYFNLVLTNVAAGDVQSVISGSSGTGMPMSRNWG 180

DB 141 PVSFRVPCVKKGGIRFTNGHSYFNLVLTNVAAGDVRSISIKSGRTGMPMSRNMG 200
 OY 181 NMOSNSYLDGQSLSFQVAVSDGRTVTSNNVPAAGMFCGTFEGGQF 226
 DB 201 NMOSNMFLDGQSLSFQVAVSDGRTVTSNNVPAHGMFCGTFEGGQF 246

RESULT 5
 OY46J0 ID 0946J0 PRELIMINARY: PRT: 246 AA.

AC 0946J0: 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DB ALPHA-EXPANSIN.
 GN EXP4.
 OS Oryza sativa (Rice).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NC NCB1_TaxID=4530;
 RN [1]
 RX MEDLINE=21521099; PubMed=11641069;
 RA Lee Y., Choi D., Kende H.;
 RT "Expansins: ever-expanding numbers and functions.";
 RL Curr. Opin. Plant Biol. 4:527-532(2001).
 DR EMBL: AF394545; MBL24481.1; -
 SQ SEQUENCE 246 AA; 25884 MW; DFAA1224D8A3F9A0 CRC64;

Query Match 87.2%; Score 1096.5; DB 10; Length 246;
 Best Local Similarity 86.7%; Pred. No. 2.7e-91;
 Matches 196; Conservative 8; Mismatches 21; Indels 1; Gaps 1;
 OY 2 YSSMSAHATFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFPNDGAACRSCYELR 60
 DB 21 YGSMQSAHATFYGGDASGTMGACGYNLYSTGYCTNTAALSTALFNDGAACGSCYELR 80
 OY 61 CDNDGQMLPGSVYVATNLCPPNYALPNDGGMCPRRPHDMAEPALQIGYRAGIY 120
 DB 81 CDNAGSSCLPGSVYVATNLCPPNYALPNDGGMCPRRPHDMAEPALQIGYRAGIY 140
 OY 121 PVSFRVPCVKKGGIRFTNGHSYFNLVLTNVAAGDVRSISIKSGRTGMPMSRNMG 180
 DB 141 PVSFRVPCVKKGGIRFTNGHSYFNLVLTNVAAGDVRSISIKSGRTGMPMSRNMG 200
 OY 181 NMOSNSYLDGQSLSFQVAVSDGRTVTSNNVPAAGMFCGTFEGGQF 226
 DB 201 NMOSNMFLDGQSLSFQVAVSDGRTVTSNNVPAHGMFCGTFEGGQF 246

RESULT 6
 OY46J0 ID 0946J0 PRELIMINARY: PRT: 252 AA.
 AC 0946J0: 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DB EXPANSIN.
 GN EXP2.
 OS Festuca pratensis.
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; Pooidae;
 OC Poaceae; Festuca.
 NC NCB1_TaxID=4608;
 RN [1]
 RX SEQUENCE FROM N.A.
 RC STRAIN=CV. PREEST.; TISSUE=LEAF ELONGATION ZONE;
 RA MEDLINE=2137433; PubMed=11485205;
 RL Reidy B., McQueen-Mason S., Noesberger J., Fleming A.;
 RT "Differential Expression of alpha- and beta-expansin genes in the
 elongating leaf of Festuca pratensis.";

RL Plant Mol. Biol. 46:491-504(2001).
 DR EMBL: AJ276007; CAC06433.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 252 AA; 26544 MW; BE8624E919F42238 CRC64;

Query Match 84.7%; Score 1065; DB 10; Length 252;
 Best Local Similarity 85.1%; Pred. No. 1.9e-88;
 Matches 194; Conservative 10; Mismatches 22; Indels 2; Gaps 2;

OY 1 DYSSMSAHATFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFPNDGAACRSCYEL 59
 DB 25 DYSSMSAHATFYGGDASGTMGACGYNLYSTGYCTNTAALSTALFNDGAACGSCYEL 84
 OY 60 RCDND-GQWCLPGSVYVATNLCPPNYALPNDGGMCPRRPHDMAEPALQIGYRAGI 118
 DB 85 KDAVAGTTCRAGSITVATNLCPPNYALPNDGGMCPRRPHDMAEPALQIGYRAGI 144
 OY 119 IVPVSFRVPCVKKGGIRFTNGHSYFNLVLTNVAAGDVRSISIKSGRTGMPMSRNMG 178
 DB 145 IVPVSFRVPCVKKGGIRFTNGHSYFNLVLTNVAAGDVRSISIKSGRTGMPMSRNMG 204
 OY 179 GQMSNSYLDGQSLSFQVAVSDGRTVTSNNVPAAGMFCGTFEGGQF 226
 DB 205 GQMSNMFLDGQSLSFQVAVSDGRTVTSNNVPAHGMFCGTFEGGQF 252

RESULT 7
 OY46J0 ID 082093 PRELIMINARY: PRT: 254 AA.
 AC 082093: 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DB EXPANSIN.
 GN PA-EXPI.
 OS Prunus armeniaca (Apricot).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots; Rosidae;
 OC Eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 NC NCB1_TaxID=36596;
 RN [1]
 RX SEQUENCE FROM N.A.
 RC STRAIN=BERGERON; TISSUE=MESOCARP PLUS EXOCARP;
 RA Mbeguie A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.;
 RT "Molecular cloning and nucleotide sequence of expansin 1 (Pa-Exp1)
 from apricot fruit.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U93167; AAC33529.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen.1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 254 AA; 27264 MW; 88068D75932FD0E1 CRC64;

Query Match 82.1%; Score 1031.5; DB 10; Length 254;
 Best Local Similarity 79.7%; Pred. No. 2.1e-85;
 Matches 181; Conservative 16; Mismatches 29; Indels 1; Gaps 1;
 OY 1 DYSSMSAHATFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFPNDGAACRSCYEL 59
 DB 28 DYSSMSAHATFYGGDASGTMGACGYNLYSTGYCTNTAALSTALFNDGAACGSCYEL 87
 OY 60 RCDNDGQMLPGSVYVATNLCPPNYALPNDGGMCPRRPHDMAEPALQIGYRAGI 119
 DB 88 RCDNDGQMLPGSVYVATNLCPPNYALPNDGGMCPRRPHDMAEPALQIGYRAGI 147
 OY 120 IVPVSFRVPCVKKGGIRFTNGHSYFNLVLTNVAAGDVRSISIKSGRTGMPMSRNMG 179
 DB 148 IVPVSFRVPCVKKGGIRFTNGHSYFNLVLTNVAAGDVRSISIKSGRTGMPMSRNMG 207
 OY 180 QMSNSYLDGQSLSFQVAVSDGRTVTSNNVPAAGMFCGTFEGGQF 226

Db 208 QNMOSNNYLNQSLSFQVTTSDGRTVTSNNVAPGNMFGQTFSSGQF 254

RESULT 8

09FUM3 PRELIMINARY; PRT; 254 AA.

AC 09FUM3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EXPANSIN 1.
GN EXP1 OR EXP2.
OS Prunus avium (cherry), and
OS Prunus cerasus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=42229, 140311;

RP SEQUENCE FROM N.A.
RC SPECIES=P.avium;
RA Wu Z., Wiersma P.A.;
RT "Differential Expression of Expansin Genes Isolated from Sweet Cherry (Prunus avium L.) During Fruit Ripening."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RP SPECIES=P.cerasus; TISSUE=RIPENING FRUIT;
RA Yoo S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.;
RT "Coordinated expression of genes encoding expansins and other cell wall-modifying enzymes is associated with pectin-related changes in the cell wall during ripening of cherry (P. cerasus) fruit."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF297521; AAG13982.1; -
DR EMBL: AF350937; AAK48846.1; -
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen.1.
DR PRINTS: PR01225; EXPANSNFAMLY.
DR ProDom: PD002179; Pollen_allergen.1.
SO SEQUENCE 254 AA; 27278 MW; 953A7EB2491FDE1 CRC64;

Query Match 81.8%; Score 1028.5; DB 10; Length 254;
Best Local Similarity 79.3%; Pred. No. 3.9e-85;
Matches 180; Conservative 17; Mismatches 29; Indels 1; Gaps 1;

QY 1 DYSWQSAHATFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFPNDGACRSCYE 59
DB 28 DYCGWGAHATFYGGDASGTMGACGYGNLYSGYGTNTAALSTALFNNGLSCGSCYE 87
QY 60 RCDNDGQWCLPGSVTVATNLCPPNYALPNDGQWCPNPPHFDMAEPALQIGVYRAGI 119
DB 88 RCNNDPRMCRPGSITVATNFCPPNFAQNDGMCNPPLOHFDLAPALQIAYRAGI 147
QY 120 VPVSYRRVPCVKKGIRFTINGHSYFNLYLVTVNAGPGDVQSYSTGSSSTGMPMRNW 179
DB 148 VPTFRRVPCMKGIRFTINGHSYFNLYLVTVNAGADVHSYISKSRGQWPMRNMW 207
QY 180 QNMOSNYLDGQSLFQVAVSDGRTVTSNNVAPGNMFGQTFSSGQF 226
DB 208 QNMOSNYLNQSLSFQVTTSDGRTVTSNNVAPGNMFGQTFSSGQF 254

RESULT 9

09SBT1 PRELIMINARY; PRT; 253 AA.

AC 09SBT1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EXPANSIN.
GN EXP2.
OS Fragaria ananassa (Strawberry).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=3747;

RP SEQUENCE FROM N.A.
RC STRAIN=CV. CHANDLER;
RA Civeello P.M., Sabehat A., Powell A.L.T., Bennett A.B.;
RT "An expansin gene expressed in ripening strawberry fruit is auxin-independent."
RL Plant Physiol. 12:1273-1279(1999).
DR EMBL: AF159563; AAF21101.1; -
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen.1.
DR PRINTS: PR01225; EXPANSNFAMLY.
DR ProDom: PD002179; Pollen_allergen.1.
DR PROSITE: PS00626; RCCL2; UNKNOWN_1.
SO SEQUENCE 253 AA; 26887 MW; CE39CF00ADEACEF CRC64;

Query Match 81.4%; Score 1023; DB 10; Length 253;
Best Local Similarity 80.3%; Pred. No. 1.2e-84;
Matches 183; Conservative 13; Mismatches 30; Indels 2; Gaps 2;

QY 1 DY-SSWQSAHATFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFPNDGACRSCYE 58
DB 26 DYCGWGAHATFYGGDASGTMGACGYGNLYSGYGTNTAALSTALFNNGLSCGSCYE 85
QY 59 LRCNDGQWCLPGSVTVATNLCPPNYALPNDGQWCPNPPHFDMAEPALQIGVYRAGI 118
DB 86 MRCNDPRMCRPGSITVATNFCPPNFAQNDGMCNPPLOHFDLAPALQIAYRAGI 145
QY 119 VPVSYRRVPCVKKGIRFTINGHSYFNLYLVTVNAGPGDVQSYSTGSSSTGMPMRNW 178
DB 146 IYPVSRRRVPCVKKGIRFTINGHSYFNLYLVTVNAGADVHSYISKSRGQWPMRNMW 205
QY 179 QNMOSNYLDGQSLFQVAVSDGRTVTSNNVAPGNMFGQTFSSGQF 226
DB 206 QNMOSNYLNQSLSFQVTTSDGRTVTSNNVAPGNMFGQTFSSGQF 253

RESULT 10

P93493 PRELIMINARY; PRT; 232 AA.

AC P93493;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EXPANSIN (FRAGMENT).
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;

RP SEQUENCE FROM N.A.
RC TISSUE=HYPOCOTYL;
RA Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
RT "Expansins are conserved in conifers and expressed in response to exogenous auxin."
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64691; AAB40635.1; -
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen.1.
DR PRINTS: PR01225; EXPANSNFAMLY.
DR ProDom: PD002179; Pollen_allergen.1.
FT NON_TER 1

SO SEQUENCE 232 AA; 24745 MW; 1340B0573DE907CF CRC64;

Query Match 81.3%; Score 1021.5; DB 10; Length 232;
Best Local Similarity 79.1%; Pred. No. 1.5e-84;
Matches 178; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

QY 2 YSSWQSAHATFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFPNDGACRSCYELR 60

Db 7 YGWMESAHATFYGGSDASGTGACGCGNLVSGYGTNTALSTALFNDGSCGACIEMR 66
 OY 61 CNDGQWCLPGSVTVATNLCPPNYALPNDGQWGNPPRPHFMAEPALQIGYRAGIV 120
 Db 67 CNDGQWCLPGSVTVATNLCPPNYALPNDGQWGNPPRPHFMAEPALQIGYRAGIV 126
 OY 121 PVSRYRVPCKKGGIRFTINGHSYFNLYVTNNVAGPDGVOSVTKSGSSQWPMRNMGO 180
 Db 127 PILYTRVPCLRKGGIRFTVNGHSYFNLYVTNNVAGPDGVOSVTKSGSSQWPMRNMGO 186
 OY 181 NMQNSYLDGQSLSFQYAVSDGRTVTSNNVAPAGMFGQTFEGSQ 225
 Db 187 NMQNSYLDGQSLSFQYAVSDGRTVTSNNVAPAGMFGQTFEGSQ 231

RESULT 11
 O93WY1 PRELIMINARY: PRT: 253 AA.

AC O93WY1: 1
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE EXPANSIN.
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 NCBI_TaxID=3352;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=HYPOCOTYL;
 RX HUTCHISON K.W., SINGER P.B., MCINUS S., DIAZ-SALA C., GREENWOOD M.S.;
 RT "Expansins are conserved in conifers and expressed in hypocotyls in
 response to exogenous auxin."
 RL Plant Physiol. 120:827-832(1999).
 DR EMBL: AF085330; AAD47901.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 DR ProDom: PD002179; Pollen_allergen; 1.
 SQ SEQUENCE 253 AA; 27150 MW; 2675BB1569BD75D4 CRC64;

Query Match 81.3%; Score 1021.5; DB 10; Length 253;
 Best Local Similarity 79.1%; Pred. No. 1.7e-84;
 Matches 178; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

OY 2 YSSWQSAHATFYGGSDASGTGACGCGNLVSGY-TNTAALSTVLFNDGACRSCYEIR 60
 Db 28 YGWMESAHATFYGGSDASGTGACGCGNLVSGYGTNTAALSTALFNDGSCGACIEMR 87
 OY 61 CNDGQWCLPGSVTVATNLCPPNYALPNDGQWGNPPRPHFMAEPALQIGYRAGIV 120
 Db 88 CNDGQWCLPGSVTVATNLCPPNYALPNDGQWGNPPRPHFMAEPALQIGYRAGIV 147
 OY 121 PVSRYRVPCKKGGIRFTINGHSYFNLYVTNNVAGPDGVOSVTKSGSSQWPMRNMGO 180
 Db 148 PILYTRVPCLRKGGIRFTVNGHSYFNLYVTNNVAGPDGVOSVTKSGSSQWPMRNMGO 207
 OY 181 NMQNSYLDGQSLSFQYAVSDGRTVTSNNVAPAGMFGQTFEGSQ 225
 Db 208 NMQNSYLDGQSLSFQYAVSDGRTVTSNNVAPAGMFGQTFEGSQ 252

RESULT 12
 P93492 PRELIMINARY: PRT: 232 AA.
 AC P93492: 1
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE EXPANSIN (FRAGMENT).
 OS Pinus taeda (loblolly pine).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 NCBI_TaxID=3352;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=HYPOCOTYL;
 RX HUTCHISON K.W., SINGER P.B., DIAZ-SALA C., GREENWOOD M.S.;
 RT "Expansins are conserved in conifers and expressed in response to
 exogenous auxin."
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64890; AAB40634.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 DR ProDom: PD002179; Pollen_allergen; 1.
 FT NON_TER 1
 SQ SEQUENCE 232 AA; 24734 MW; 1340AF483DE0741F CRC64;

Query Match 81.2%; Score 1020.5; DB 10; Length 232;
 Best Local Similarity 78.7%; Pred. No. 1.8e-84;
 Matches 177; Conservative 19; Mismatches 28; Indels 1; Gaps 1;

OY 2 YSSWQSAHATFYGGSDASGTGACGCGNLVSGY-TNTAALSTVLFNDGACRSCYEIR 60
 Db 7 YGWMESAHATFYGGSDASGTGACGCGNLVSGYGTNTAALSTALFNDGSCGACIEMR 66
 OY 61 CNDGQWCLPGSVTVATNLCPPNYALPNDGQWGNPPRPHFMAEPALQIGYRAGIV 120
 Db 67 CNDGQWCLPGSVTVATNLCPPNYALPNDGQWGNPPRPHFMAEPALQIGYRAGIV 126
 OY 121 PVSRYRVPCKKGGIRFTINGHSYFNLYVTNNVAGPDGVOSVTKSGSSQWPMRNMGO 180
 Db 127 PILYTRVPCLRKGGIRFTVNGHSYFNLYVTNNVAGPDGVOSVTKSGSSQWPMRNMGO 186
 OY 181 NMQNSYLDGQSLSFQYAVSDGRTVTSNNVAPAGMFGQTFEGSQ 225
 Db 187 NMQNSYLDGQSLSFQYAVSDGRTVTSNNVAPAGMFGQTFEGSQ 231

RESULT 13
 O93XP2 PRELIMINARY: PRT: 253 AA.
 AC O93XP2: 1
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE EXPANSIN.
 OS Prunus cerasus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eursids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 NCBI_TaxID=140311;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=RIPENING FRUIT;
 RX YOO S.-D., GAO Z., CANTINI C., LOESCHER W., VAN NOCKER S.;
 RT "Coordinated expression of genes encoding expansins and other cell
 wall-modifying enzymes is associated with pectin-related changes in
 the cell wall during ripening of cherry (P. cerasus) fruit."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF505936; AAK48845.1;
 SQ SEQUENCE 253 AA; 26861 MW; 9C24484F14AA52CD CRC64;

Query Match 81.1%; Score 1019; DB 10; Length 253;
 Best Local Similarity 79.8%; Pred. No. 2.8e-84;
 Matches 182; Conservative 13; Mismatches 31; Indels 2; Gaps 2;

OY 1 DY-SSWQSAHATFYGGSDASGTGACGCGNLVSGY-TNTAALSTVLFNDGACRSCYEIR 58
 Db 26 DYGGWEGHATFYGGSDASGTGACGCGNLVSGYGTNTAALSTALFNDGSCGACIEMR 85
 OY 59 LRCNDGQWCLPGSVTVATNLCPPNYALPNDGQWGNPPRPHFMAEPALQIGYRAG 118

Db 86 MRCOSDKMCLPGSIIVTATNFCPPNLQSDNGMCNPLQHFDLAEPAFLQIQAQYRAG 145
 QY 119 IVPVSRVPCVKKGIRFTINGHSYFNLVLTNNVAGPGVSVSISKSGSTGQPMRSRW 178
 Db 146 IVPVSRVPCVKKGIRFTINGHSYFNLVLTNNVAGPGVSVSISKSGSTGQPMRSRW 205
 QY 179 GONNOSNYLDGSLSFQVAVSDGRTVTSNNVYPAGMOFGQTFEGGQF 226
 Db 206 GONNOSNYLDGSLSFQVAVSDGRTVTSNNVYPAGMOFGQTFEGGQF 253

RESULT 14

P93495 PRELIMINARY; PRT; 232 AA.

ID P93495
 AC P93495
 DT 01-MAY-1997 (TREMUREL. 03, Created)
 DT 01-MAY-1997 (TREMUREL. 03, Last sequence update)
 DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)
 DE EXPANSIN (FRAGMENT).
 OS Pinus taeda (loblolly pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOCOTYL;
 RA Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
 RT "Expansins are conserved in conifers and expressed in response to
 exogenous auxin."
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64893; ABA0637.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen. 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR Prodom: PD002179; Pollen_allergen. 1.
 FT NON_TER
 SQ SEQUENCE 232 AA; 24694 MW; 9238EACD9E1F6C5E CRC64;

Query Match

Best Local Similarity 80.9%; Score 1017.5; DB 10; Length 232;
 Best Local Similarity 78.7%; Pred. No. 3.4e-84;

Matches 177; Conservative 19; Mismatches 28; Indels 1; Gaps 1;

QY 2 YSMQSAHATFYGGGDSAGTGTGYNLYSTGY-TNTAALSTVLFNDGACRSCYELR 60
 Db 7 YGWMESAHATFYGGGDSAGTGTGYNLYSTGY-TNTAALSTVLFNDGACRSCYELR 66
 QY 61 CDNDGQWCLPGSVYVATNLCPPNYALPNDGCKNPPRPHFDMAEPALQIGYRAGIV 120
 Db 67 CNDGPQWCLPGSVYVATNLCPPNYALPNDGCKNPPRPHFDMAEPALQIGYRAGIV 126
 QY 121 PVSYRRVPCVKKGIRFTINGHSYFNLVLTNNVAGPGVSVSISKSGSTGQPMRSRW 180
 Db 127 PILYTRVPCVKKGIRFTINGHSYFNLVLTNNVAGPGVSVSISKSGSTGQPMRSRW 186
 QY 181 NMOSNSYLDGSLSFQVAVSDGRTVTSNNVYPAGMOFGQTFEGGQF 225
 Db 187 NMOSNSYLDGSLSFQVAVSDGRTVTSNNVYPAGMOFGQTFEGGQF 231

RESULT 15

Q9LLB2 PRELIMINARY; PRT; 245 AA.

ID Q9LLB2
 AC Q9LLB2
 DT 01-OCT-2000 (TREMUREL. 15, Created)
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
 DT 01-JUN-2001 (TREMUREL. 17, Last annotation update)
 DE EXPANSIN 2.
 OS Zinnia elegans.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
 OC Asteridae; easterids II; Asterales; Asteraceae; Asteroideae;
 OC Heliantheae; Zinnia.

OX NCBI_TaxID=34245;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20317189; PubMed-10859177;
 RA Im K.H., Cosgrove D.J., Jones A.M.;
 RT "Subcellular localization of expansin mRNA in xylem cells."
 RL Plant Physiol. 123:463-470(2000).
 DR EMBL: AF230332; AAF35901.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen. 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR Prodom: PD002179; Pollen_allergen. 1.
 SQ SEQUENCE 245 AA; 26201 MW; F65E26114C27E360 CRC64;

Query Match 80.9%; Score 1017.5; DB 10; Length 245;
 Best Local Similarity 77.9%; Pred. No. 3.6e-84;

Matches 176; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

QY 2 YSMQSAHATFYGGGDSAGTGTGYNLYSTGY-TNTAALSTVLFNDGACRSCYELR 60
 Db 20 YGWMESAHATFYGGGDSAGTGTGYNLYSTGY-TNTAALSTVLFNDGACRSCYELR 79
 QY 61 CDNDGQWCLPGSVYVATNLCPPNYALPNDGCKNPPRPHFDMAEPALQIGYRAGIV 120
 Db 80 CNDGPQWCLPGSVYVATNLCPPNYALPNDGCKNPPRPHFDMAEPALQIGYRAGIV 139
 QY 121 PVSYRRVPCVKKGIRFTINGHSYFNLVLTNNVAGPGVSVSISKSGSTGQPMRSRW 180
 Db 140 PILYTRVPCVKKGIRFTINGHSYFNLVLTNNVAGPGVSVSISKSGSTGQPMRSRW 199
 QY 181 NMOSNSYLDGSLSFQVAVSDGRTVTSNNVYPAGMOFGQTFEGGQF 226
 Db 200 NMOSNSYLDGSLSFQVAVSDGRTVTSNNVYPAGMOFGQTFEGGQF 245

Search completed: October 11, 2002, 14:59:42

Job time : 20.5144 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:50:30 : Search time 5.83764 Seconds
(without alignments)
1499.000 Million cell updates/sec

Title: US-09-896-301-6
Perfect score: 1257
Sequence: 1 DYSSWQSAHATFYGGDASG.....SNNVVPAGWQPGQTFEGGQF 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	232	18.5	246	1	MPCL_CYNDA
2	214.5	17.1	263	1	MP1L_LOLPR
3	207.5	16.5	269	1	MP1L_PHAQ
4	206.5	16.4	265	1	MP1L_HOLLA
5	203	16.1	191	1	MP2L_MAIZE
6	201.5	16.0	263	1	MP1L_PHLPR
7	175	13.9	263	1	MPOL_PRTSA
8	105.5	8.4	418	1	GUN5_TRIRE
9	93	7.4	418	1	GUN2_TRIRE
10	92.5	7.4	466	1	NA95_HUMAN
11	90.5	7.2	333	1	CART_MOUSE
12	87	6.9	766	1	DP24_HUMAN
13	86.5	6.9	1246	1	YMW2_CAEEL
14	85	6.8	571	1	FLA1_CAMJE
15	84.5	6.7	1176	1	CICB_BACTG
16	84	6.7	3011	1	POLG_HCVI
17	83.5	6.6	513	1	GUX1_TRIVI
18	83.5	6.6	747	1	GUND_CELFI
19	83	6.6	571	1	FLB1_CAMJE
20	82.5	6.6	574	1	FLA3_CAMJE
21	82.5	6.6	574	1	FLB3_CAMJE
22	82.5	6.5	1193	1	LMG2_HUMAN
23	81.5	6.5	1376	1	CRBH_HUMAN
24	81.5	6.5	3695	1	LMAS_HUMAN
25	81	6.4	430	1	SHU2_ECOLI
26	81	6.4	433	1	SHU6_ECOLI
27	81	6.4	442	1	SHU3_ECOLI
28	81	6.4	444	1	SHU4_ECOLI
29	81	6.4	444	1	SHU5_ECOLI
30	81	6.4	456	1	SHU7_ECOLI
31	81	6.4	474	1	SHU1_ECOLI
32	81	6.4	1173	1	TSR1_XENLA
33	80	6.4	677	1	SPB7_DICDI

34	80	6.4	703	1	COAT_SMSV4	P36285	san m...
35	80	6.4	1429	1	L112_CAEEL	P14585	caenorhabd
36	80	6.4	3718	1	LMAS_MOUSE	O61001	mus musculu
37	79.5	6.3	852	1	CSG_HALNA	P08198	halobacteri
38	79.5	6.3	1385	1	YMS3_CAEEL	P34501	caenorhabd
39	79.5	6.3	2437	1	NOTC_BRARE	P46530	brachydanio
40	79	6.3	213	1	XYNA_BACSU	P18429	bacillus su
41	78.5	6.2	181	1	GUN_MYTED	P82186	mytilus edu
42	78.5	6.2	513	1	GUX1_TRIRE	P00725	trichoderma
43	78.5	6.2	642	1	NA95_MOUSE	O9F017	mus musculu
44	78.5	6.2	1286	1	AIDA_ECOLI	O03155	escherichia
45	78	6.2	213	1	XYNA_BACCI	P09850	bacillus ci

ALIGNMENTS

RESULT 1
ID MPCL_CYNDA STANDARD; PRT; 246 AA.
AC O04701:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Major pollen allergen Cyn d 1.
GN CYNDL.
OS Cynodon dactylon (Bermuda grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Chloridoideae; Cynodonteae; Cynodon.
OX NCBI_TaxID=28909;
RN [1]
RP TISSUE=POLLEN; AND PARTIAL SEQUENCE.
RC MEDLINE=96347957; PubMed=8757211.
RA Smith P.M., Suphloglu C., Griffith I.J., Theriault K., Knox R.B.,
RA Singh M.B.;
RT "Cloning and expression in yeast Pichia pastoris of a biologically
RT active form of Cyn d 1, the major allergen of Bermuda grass pollen";
RL J. Allergy Clin. Immunol. 98:331-343(1996).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
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CC
CC EMBL: S83343; AAB50734.2; -.
CC DR HSSP: P43214; IMHO.
CC DR InterPro: IPR000882; Pollen_allergen.
CC Pfam: PF01357; Pollen_allergen; 1.
CC PRINTS: PR01225; EXPANSIN_FAMLY.
CC DR PRODOM: PD002179; Pollen_allergen; 1.
CC DR PROSITE: PS50843; EXPANSIN_CBD; 1.
CC DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen.
FT DOMAIN 39 145 EXPANSIN-LIKE EG45.
FT DOMAIN 159 240 EXPANSIN-LIKE CBD.
FT CARBOHD 9 N-LINKED (GLCNAC...) (POTENTIAL).
SO SEQUENCE 246 AA; 26888 MW; 43D8442DBA58322 CRC64;
Query Match 18.5%; Score 232; DB 1; Length 246;
Best Local Similarity 28.3%; Pred. No. 6e-13;
Matches 69; Conservative 37; Mismatches 96; Indels 42; Gaps 10;
Qy 3 SWSQSAHATFYGG--GDASGTMGTCGYNLYSTGYTN-TAALSTVLFNDGACRSCYE 58

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Db 16 SKMIEARATFYGSNPRCAAPDDHGGAGYKVDVDPKPPDCMTACGNEPIFKDGLCCFRACE 75
Qy 59 LRCNDGOWCLPGSVYVYATATNLCPNNALPNDGGMKCNPPRPDMMAPFAFLQI----- 113
Db 76 IKCEPEVE-CGGEFVLVKIT-----DKNYEHIAAYHEDLSGKAFGAAKKGOE 122
Qy 114 --VYRACIVPYSRRVPCVKKGIRFTIN---GHSYFNLVLYNNVAGPDVOSVSIK-G 166
Db 123 DKLKAGGLTLQFRVCKYPSGKIFHIEKSNHLYLVYXAGDGNVAVDILKPR 182
Qy 167 SGTGMQPSRNMGNOMQ--SNSYVDSGLSFQVAVSDGRVTSNNVYPAGM----- 215
Db 183 DSDDEFIMKSSWGAIRIDPKPLKG-PFSIRLTSEGAHLVODDIPAMWKPDVYTSK 241
Qy 216 -QFG 218
Db 242 LQFG 245

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RESULT 2

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MPIL_LOLPR STANDARD; PRT; 263 AA.

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AC P14946; P19964;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Pollen allergen Lol p 1 precursor (Lol p 1) (Allergen R7).
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Lolium.
OX NCBI_TaxID=4522;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=90375479; PubMed=1697854;
RA Perez M., Ishioka G.Y., Walker L.E., Chesnut R.W.;
RT "cDNA cloning and immunological characterization of the rye grass
RT allergen Lol p 1."
RL J. Biol. Chem. 265:16210-16215(1990).
RN [2]

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RP SEQUENCE FROM N.A. AND SEQUENCE OF 24-48.
RC TISSUE=PolLEN;
RX MEDLINE=91160716; PubMed=2001733;
RA Griffith I.J., Smith P.M., Pollock J., Theerakulpisut P.,
RA Avoglu A., Davies S., Hough T., Singh M.B., Simpson R.J., Ward L.D.,
RA Knox R.B.;
RT "Cloning and sequencing of Lol p1, the major allergenic protein of
RT rye-grass pollen."
RL FEBS Lett. 279:210-215(1991).
RN [3]

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RP SEQUENCE OF 24-53.
RC TISSUE=PolLEN;
RX MEDLINE=86242068; PubMed=3718469;
RA Cortam G.P., Moran D.M., Standring R.;
RT "Physicochemical and immunochemical characterization of allergenic
RT proteins from rye-grass (Lolium perenne) pollen prepared by a rapid
RT and efficient purification method."
RL Biochem. J. 234:305-310(1986).
RN [4]

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RP SEQUENCE OF 236-263.
RX MEDLINE=89364850; PubMed=2475768;
RA Esch R.E., Klapper D.G.;
RT "Isolation and characterization of a major cross-reactive grass group
RT I allergenic determinant."
RL Mol. Immunol. 26:557-561(1989).
RN [5]

```

```

CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P 1 FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.

```

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DR EMBL: M57474; AAA63279.1; -
DR EMBL: M57476; AAA63278.1; -
DR PIR: A23341; A23341.
DR PIR: B37881; B37881.
DR PIR: S13614; S13614.
DR HSP: P43214; IWHO.
DR InterPro: IP000882; pollen_allergen.
DR Pfam: PF01357; Pollen allergen; 1.
DR PRINTS: PR002179; Pollen allergen; 1.
DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 263
FT DOMAIN 61 167
FT DOMAIN 181 262
FT CARBOHYD 32 32
FT VARIANT 68 68
FT VARIANT 177 177
FT VARIANT 210 210
FT VARIANT 246 246
FT CONFLICT 28 28
FT CONFLICT 31 31
FT CONFLICT 48 48
SQ SEQUENCE 263 AA; 28438 MW; 7675896F279C88C9 CRC64;

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Query Match 17.1%; Score 214.5; DB 1; Length 263;
Best local Similarity 29.1%; Pred. No. 2e-11;
Matches 67; Conservative 32; Mismatches 98; Indels 33; Gaps 11;

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Qy 5 WQSAHATFYGGGADSGTM--GGTGYGNLYSGYTN-TAALSTVLFNDGACRSCYEELK 61
Db 41 WLDKSTWGTGKPRGAGPRKNGAGCYKNDKAPFNOMTCGNTPIFKDRGSGSCFEIKC 100
Qy 62 DNDGOWCLPGSVYVYATATNLCPNNALPNDGGMKCNPPRPDMMAPFAFLQI-----G 113
Db 101 TKP-ESCSGEFAVYVYIT-----DDNE--EPIDYHFDLSGHAFGSAKKAGEQN 146
Qy 114 VYRACIVPYSRRVPCVKKGIRFTINGHSYFN---LVLYNNVAGPGVOSVSIKGSST 169
Db 147 VSAGELELQFRVCKYPSGKIFHIEKASPNYALILVYDGDGVAVVDIKRKG 206
Qy 170 G-WQPSRNMGNOMQSN--YLDGOSLSFQVAVSDGRVTSNNVYPAGM 216
Db 207 DKWIELKESWGAIRIDTPDKLG--PFTVRYTTEGSKSEFEDVIAPEGK 255

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RESULT 3

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MPAL_PHAQ STANDARD; PRT; 269 AA.

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AC Q41260;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Major pollen allergen Pha a 1 precursor (Pha a 1).
OS Phalaris aquatica (Canary grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Phalaris.
OX NCBI_TaxID=28479;
RN [1]

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```

RP SEQUENCE FROM N.A.
RC TISSUE=PolLEN;
RX MEDLINE=96105569; PubMed=8564724;
RA Suphlogin C., Singh M.B.;

```

RT "Cloning, sequencing and expression in *Escherichia coli* of Pha a 1
RT and four isoforms of Pha a 5, the major allergens of canary grass
RT pollen";
RL Clin. Exp. Allergy 25:853-865(1995).
RN (2)
RP SEQUENCE OF 30-49.
RA MEDLINE-93319091; PubMed-7687099;
RA Suppliglu C., Singh M.B., Simpson R.J., Ward L., Knox R.B.;
RT "Identification of canary grass (Phalaris aquatica) pollen allergens
RT by immunoblotting: IgE and IgG antibody-binding studies";
RL Allergy 48:273-281(1993).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLEGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S80654; AAB35984.1; -.
DR HSSP: P43214; IMHO.
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSIN-FAMILY.
DR PRODOM: PD002179; Pollen_allergen; 1.
DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 269 MAJOR POLLEN ALLERGEN PHA A 1.
FT DOMAIN 67 173 EXPANSIN-LIKE EG45.
FT DOMAIN 187 268 EXPANSIN-LIKE CBD.
FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 37 37 P -> G (IN REF. 2).
SQ SEQUENCE 269 AA; 29011 MW; 05883A458ACE877E CRC64;

Query Match 16.5%; Score 207.5; DB 1; Length 269;
Best Local Similarity 28.3%; Pred. No. 8.1e-11;
Matches 65; Conservative 34; Mismatches 98; Indels 33; Gaps 11;

QY 5 WQSAHATFYGGDASGTM--GTCGYGNLYSTGYTN-TAALSTVLFNDGAACRSCEYLRC 61
DB 47 WLDKSTWYGRKPTGAGPKDNGAGCYKDYDKAPFNGMTCGCGNPIPKDRCGSCFELKC 106
QY 62 DNDGMCPLPGSVTVTATNLCPNRYALPNDGCGCNPPRP-HFDMAEPALQI-----G 113
DB 107 SKP-ESCSGEPYTVHIT-----DDNE--EPIDAPYHFDLSGHAFSGMAKKGEEN 152
QY 114 VVRAGIYPSYRVRPCVKKKGIRFTIN---GHSYFNLYLVTVWAGPDVOSYSKGSST 169
DB 153 VRAGLELEDFRRVCKKYPDGTKEFHEKGSNPYLLALLVYDGDVAVANDIKERK 212
QY 170 G-WQPSRMWGMQMSNS--YLDGQSLSFQVAVSDGRTVTSNNVPAQMGQ 216
DB 213 DKMTELKESWGLMIRIDTPDKLTG-PFTVAYTTEGGTKAEFEVDIPEGWK 261

RESULT 4
MPH1_HOLLA
ID MPH1_HOLLA STANDARD; PRT; 265 AA.
AC P43216; Q39975;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Major pollen allergen Hol 1 precursor (Hol 1 I) (Hol 1.1.0101 and
DE 1.0102).
OS Holcus lanatus (Velvet grass).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Holcus.
OX NCBI_TaxID=29679;
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN-CV. AVENEA; TISSUE=pollen;
RA Schramm G.D., Bufe A., Becker W.M., Schlaak M.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE OF 18-265 FROM N.A.
RC STRAIN-CV. AVENEA; TISSUE=pollen;
RA Schramm G.D., Bufe A., Petersen A., Haas H., Schlaak M., Becker W.M.;
RT "Mapping of IgE-binding epitopes on the recombinant major group 1
RT allergen of velvet grass pollen, Phol 1.1";
RL J. Allergy Clin. Immunol. 99:781-787(1997).
RN (3)
RN CHARACTERIZATION.
RP STRAIN-CV. AVENEA; TISSUE=pollen;
RC MEDLINE-96319506; PubMed-8768803;
RA Schramm G.D., Petersen A., Bufe A., Schlaak M., Becker W.M.;
RT "Identification and characterization of the major allergens of velvet
RT grass (Holcus lanatus), Hol 1.1 and Hol 1.5";
RL Int. Arch. Allergy Immunol. 110:354-363(1996).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLEGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
CC -----
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CC -----
DR EMBL: Z27084; CAA81610.1; -.
DR EMBL: Z68893; CAA93121.1; -.
DR HSSP: P43214; IMHO.
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSIN-FAMILY.
DR PRODOM: PD002179; Pollen_allergen; 1.
DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 265 MAJOR POLLEN ALLERGEN HOL 1.1.
FT DOMAIN 63 169 EXPANSIN-LIKE EG45.
FT DOMAIN 183 264 EXPANSIN-LIKE CBD.
FT VARIANT 103 103 T -> S (IN HOL 1.1.0102).
SQ SEQUENCE 265 AA; 28590 MW; 1FE23B3BE198AD6D CRC64;

Query Match 16.4%; Score 206.5; DB 1; Length 265;
Best Local Similarity 27.1%; Pred. No. 9.7e-11;
Matches 64; Conservative 39; Mismatches 100; Indels 33; Gaps 11;

QY 5 WQSAHATFYGGDASGTM--GTCGYGNLYSTGYTN-TAALSTVLFNDGAACRSCEYLRC 61
DB 43 WLDKSTWYGRKPTGAGPKDNGAGCYKDYDKAPFNGMTCGCGNPIPKDRCGSCFELKC 102
QY 62 DNDGMCPLPGSVTVTATNLCPNRYALPNDGCGCNPPRP-HFDMAEPALQI----- 113
DB 103 TRP-ESCSGEPYTVHIT-----DDNE--EPIDAPYHFDLSGHAFSGMAKKGEEN 148
QY 114 VVRAGIYPSYRVRPCVKKKGIRFTIN---GHSYFNLYLVTVWAGPDVOSYSKGSST 169
DB 149 VRAGLELEDFRRVCKKYPDGTKEFHEKGSNPYLLALLVYDGDVAVANDIKERK 208
QY 170 G-WQPSRMWGMQMSNS--YLDGQSLSFQVAVSDGRTVTSNNVPAQMGQ 222
DB 170 G-WQPSRMWGMQMSNS--YLDGQSLSFQVAVSDGRTVTSNNVPAQMGQ 222

Db 209 DKWIELESGWAGWVRVDTPKLIG-PPTVRYTEGGTKEADYIPEGWKADTAYE 263

RESULT 5

MPZ1_MAIZE STANDARD: PRT: 191 AA.

AC 007154;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Pollen allergen Zea m 1 (Zea m 1).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Pollen;

RA Broadwater A.H., Rubinstein A.L., Chay C.H., Klapper D.G.,

RA Redinger P.A.;

RT "Zea m1, the maize homolog of the allergen-encoding Lol pi gene of

RT rye grass."

RL Gene 131:227-230(1993).

CC -1- TISSUE SPECIFICITY: POLLEN TISSUE.

CC -1- DEVELOPMENTAL STAGE: EXPRESSION LOW BEFORE AND HIGH AFTER

CC POLLEN MITOSIS.

CC -1- DISEASE: CAUSES MAIZE POLLEN ALLERGY.

CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.

CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.

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CC or send an email to license@isb-sib.ch).

CC EMBL: L14271; AAA33496.1; -

DR PIR: JCI524; JCI524.

DR HSSP: P43214; IWHO.

DR MaizeDB: 65840; -

DR InterPro: IPR000882; Pollen_allergen.

DR Pfam: PF01357; Pollen_allergen. 1.

DR PRINTS: PR01225; EXPANSINFAMILY.

DR ProDom: PD002179; Pollen_allergen; 1.

DR PROSITE: PS50843; EXPANSIN_CBD; 1.

DR PROSITE: PS50842; EXPANSIN_EG45; 1.

KW Allergen; Multigene family.

FT DOMAIN 1 91 EXPANSIN-LIKE EG45.

FT DOMAIN 105 186 EXPANSIN-LIKE CBD.

SQ SEQUENCE 191 AA; 21362 MW; 6E2A9DF921C45C63 CRC64;

Query Match 16.1%; Score 203; DB 1; Length 191;

Best Local Similarity 30.6%; Pred. No. 1.4e-10;

Matches 59; Conservative 29; Mismatches 75; Indels 30; Gaps 9;

QY 39 TAAISTVLENDGACRCSCYELRCNDGQWCLPGSVYTYATNLCPPNVALPNDGQWGNPP 98

Db 2 TACGNVPIFKKGGCGSCYERCKEPE-CGQNPVTFEITDM--NY-----EPI 47

QY 99 RP-HFDMAEPAF-----LQIGYRAGIVPVSYRPPVCKKGGIRFTINGHSYFN---- 146

Db 48 APYHFDLSGKAFGLAPGLNDKLRHGGIMDYFRYRRCYTPAGQKLVFIEEGKGNPVY 107

QY 147 LVLTAVAGPDVQSVSIKGS-STGQPMRNRNQMNQNS--YLDQSLSFQVAVSDGR 203

Db 108 AVLVKFAVADGDDIYLMELQKLSAEWKPKMLSMGAIWRMDTAKATKG-PSIRITSESGK 166

QY 204 TVTISNNVVPAGWQ 216

Db 167 KYIAKDIIPANMR 179

RESULT 6

MPPI_PHLPR STANDARD: PRT: 263 AA.

AC P43213;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Pollen allergen Phl p 1 precursor (Phl p 1).
GN PHLPI.
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Poace; Phleum.
OX NCBI_TaxID=15957;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Pollen;

RA MEDLINE=95015525; PubMed=7930302;

RA Laffer S., Valenta R., Vrtala S., Susani M., van Ree R., Kraft D.,

RA Scheiner O., Duchene M.;

RT "Complementary DNA cloning of the major allergen Phl p 1 from timothy

RT grass (Phleum pratense); recombinant Phl p 1 inhibits IgE binding to

RT group I allergens from eight different grass species.";

RL J. Allergy Clin. Immunol. 94:689-698(1994).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.

CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.

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CC or send an email to license@isb-sib.ch).

CC EMBL: X78813; CAA55390.1; -

DR HSSP: P43214; IWHO.

DR InterPro: IPR000882; Pollen_allergen.

DR Pfam: PF01357; Pollen_allergen. 1.

DR PRINTS: PR01225; EXPANSINFAMILY.

DR ProDom: PD002179; Pollen_allergen; 1.

DR PROSITE: PS50843; EXPANSIN_CBD; 1.

DR PROSITE: PS50842; EXPANSIN_EG45; 1.

KW Allergen; Glycoprotein; Signal; Multigene family.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 263 POLLEN ALLERGEN PHL P 1.

FT DOMAIN 61 167 EXPANSIN-LIKE EG45.

FT DOMAIN 181 262 EXPANSIN-LIKE CBD.

FT CARBOHYD 32 32 N-LINKED (GLCNAc...) (POTENTIAL).

SQ SEQUENCE 263 AA; 28457 MW; 040BA249C17BC048 CRC64;

Query Match 16.0%; Score 201.5; DB 1; Length 263;

Best Local Similarity 26.7%; Pred. No. 2.6e-10;

Matches 63; Conservative 39; Mismatches 101; Indels 33; Gaps 11;

QY 5 WQSAHATYGGGDAGSTM--GGTCGIGNLYSTGYTN-TAAISTVLEPNDGACRCSCYELRC 61

Db 41 WLDKASTWGWKPTGAGPKNDGCGCKYDVKPPFSQMTGCGTPTFKSGCGSCFETKC 100

QY 62 DNDGQWCLGSVYTYTNTLCPPNVALPNDGQWGNPPR-HFDMAEPAFLOIG----- 113

Db 101 TKP-EACSGEPVVVHT-----DENE--EPYIAPHDLGSHAFGAANKGDEQK 146

QY 114 VYRAGIVPVSYRPPVCKKGGIRFTIN--GHSYFNILVYTNVAGPGVQSVSIKGSST 169

Db 147 LRSAGLELQFRYKCKYEDGKTYTFHYVEKSGSNPNVALLVYVAGDGDVAVVDIKESGK 206

Oy 170 G-WQPMRNMGMQMSNS--YLDGSLSPQVAVSDGRVTSTNNVYPAGMFCOTEE 222
Db 207 DKWIELKESMGALWRTDTRDKLTG--PFTVRYTTEGSTKTEADVDYIEGKAKDTSTY 261

RESULT 7
ID MPOL_ORYSA STANDARD: PRT: 263 AA.

AC 040638;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DR Major pollen allergen Ory s 1 precursor (Ory s I).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN SEQUENCE FROM N.A.
RC TISSUE=anther;
RA MEDLINE=96069591; PubMed=7590339;
RA Xu H., Theerakulpisut P., Goulding N., Suphloglu C., Singh M.B.,
Bhalla P.L.;
RT "Cloning, expression and immunological characterization of Ory s 1,
the major allergen of rice pollen.";
RL Gene 164:255-259(1995).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MATURE ANTHERS BUT NOT IN
VEGETATIVE OR OTHER FLORAL TISSUES.
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLEGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSTIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSTIN-LIKE CBD DOMAIN.
CC
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CC
CC EMBL: U31771; AA86533.1; -
DR HSSP: P43214; IMHO.
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen.1.
DR PRINTS: PR01225; EXPANSINFAMLY.
DR PRODOM: PD002179; Pollen_allergen.1.
DR PROSITE: PS50843; EXPANSTIN_CBD.1.
DR PROSITE: PS50842; EXPANSTIN_EG45.1.
KW Allergen; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 263
FT DOMAIN 61 164 MAJOR POLLEN ALLERGEN ORY S 1.
FT DOMAIN 178 259 EXPANSTIN-LIKE EG45.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 263 AA; 28497 MW; BICSF24EA398D60 CRC64;

Query Match 13.9%; Score 175; DB 1; Length 263;
Best Local Similarity 25.7%; Pred. No. 4.7e-08;
Matches 53; Conservative 37; Mismatches 82; Indels 34; Gaps 10;

Oy 23 GGTGCGNLYSTGTN-TALSLVLENDGAACSCYELRCNDGCMCLPESVYVATNLC 81
Db 61 GGAGGVADVAKAPPLGNNSGNDPIFDKGGCCSCFEIKSKP-EACSDKPALIHVTDM- 118
Oy 82 PPNVALLNDGCMNPRP-----HFDMAEPALDQIG-----VYRAGTVPVSRVPCVKK 133
Db 119 -----NDE-----PLAAVHFDLISGLAMKDGDEELRAGAGIITDQFRYKCKYPA 163
Oy 134 GIREFTIN-----GHISYFNLVLTNAGPCDVQSVSIK-GSSGTGQPMRNMGMQMSNS-- 186

Db 164 DTKITFHEKASNPNTALLVKVVAGDGVVEIKEKSGEEMKALKESMGALWRTDTRPK 223
Oy 187 YLDGSLSPQVAVSDGRVTSTNNVYP 212
Db 224 PLKG-PFSVRYTTEGARSSAEDAIP 248

RESULT 8
ID GUNS_TRIE STANDARD: PRT: 242 AA.

AC P4317;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DR Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)
DE (Cellulase V) (EC V).
GN EGL5.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN SEQUENCE FROM N.A.
RC STRAIN=QM9414 / RUT C-30;
RC MEDLINE=95075308; PubMed=7984103;
RA Saloheimo A., Henriksas B., Hoffren A.-M., Telemann O., Penttilae M.;
RT "A novel, small endoglucanase gene, egl5, from Trichoderma reesei
isolated by expression in yeast.";
RL Mol. Microbiol. 13:219-228(1994).
CC -1- CATALYTIC ACTIVITY: Endohydrolasts of 1,4-beta-D-glucosidic
linkages in cellulose.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY K (FAMILY 45 OF GLYCOSYL
HYDROLASES).
CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBU).
CC
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CC
CC EMBL: Z33381; CAA83846.1; -
DR HSSP: P00725; 2CBH.
DR InterPro: IPR000254; CBD_fungal.
DR InterPro: IPR000334; Glyco_hydro_45.
DR Pfam: PF00734; CBD_1.1.
DR Pfam: PF02015; Glyco_hydro_45.1.
DR PRODOM: PD001821; CBD_fungal.1.
DR SMART: SM00236; FCBD.1.
DR PROSITE: PS00562; CBD_FUNGAL.1.
DR PROSITE: PS50842; EXPANSTIN_EG45.1.
DR PROSITE: PS01140; GLYCOSYL_HYDROL_45.1.
KW Cellulose degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 17
FT CHAIN 18 242
FT ACT_SITE 27 27 ENDOGLUCANASE V.
FT ACT_SITE 134 134 NICLOPHILE (BY SIMILARITY).
FT ACT_SITE 134 134 PROTON DONOR (BY SIMILARITY).
FT DOMAIN 18 182 CATALYTIC.
FT DOMAIN 183 205 PRO/SER-RICH (LINKER).
FT DOMAIN 206 242 CELLULOSE-BINDING (BY SIMILARITY).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 213 230 BY SIMILARITY.
FT DISULFID 224 240 BY SIMILARITY.
SQ SEQUENCE 242 AA; 24411 MW; CC033FC51326C71D CRC64;

Query Match 8.4%; Score 105.5; DB 1; Length 242;
Best Local Similarity 26.9%; Pred. No. 0.037;
Matches 43; Conservative 18; Mismatches 74; Indels 53; Gaps 11;

Oy 3 SSWQSHAFYFGS-----GDASGTMGTCGYGN-LYSTGTNTALSLVLEND----- 49

Db 16 SAYATTTRYDGGEGACGCGSSGAPFMOLGNGVY-----TAAGSQALETAGASW 69
 QY 50 -GAACRSCYELR-----CDNDGQMCPLPG-SVYTAATNLCPPNVALPNDGCGMCPNRP- 100
 Db 70 CGAGCGKCYQLTSTGQAFCCSSCGTGAAGOSIYVNTNLCD-----NNGNQMOC-----PV 120
 QY 101 -----HFDMAEPALQIGYRAGIVPVSRYRVP 129
 Db 121 VGTNNGYGYSHFDI-----MAONEIFGDNVY-VDPEFIAC 155

RESULT 9
 GUN2_TRIE STANDARD; PRT; 418 AA.
 AC P07982;
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Endoglucanase EG-II precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (cellulase).
 GN EGL2 OR EGLI.
 OS Trichoderma reesei (Hypocrea jecorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Hypocreaceae; Hypocrea.
 OX NCBI_TaxID=51453;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VTT-D-80133;
 RX MEDLINE=88255850; PubMed=3384334;
 RA Saloheimo M., Lehtovaara P., Penttilae M., Teeri T.T., Staahlberg J.,
 Johansson G., Pettersson G., Claysens M., Tomme P., Knowles J.K.C.;
 RT "EGLI, a new endoglucanase from Trichoderma reesei: the
 RT characterization of both gene and enzyme."; Gene 63:11-21(1988).
 RL [2]
 RN [2]
 RP ACTIVE SITE GLU-350.
 RX MEDLINE=93131031; PubMed=8093602;
 RA Macarion R., van Beeumen J., Henriassat B., de la Mata I.,
 RA Claeysens M.;
 RT "Identification of an essential glutamate residue in the active site
 RT of endoglucanase III from Trichoderma reesei."; FEBS Lett. 316:137-140(1993).
 RL [2]
 CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
 CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
 CC (1) EXOCELLULOBIOLYASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
 CC (2) EXOCELLULOBIOLYASES THAT CUT THE DISSACCHARIDE CELLULOSE
 CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLULOSE AND OTHER
 CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M19373; AAA34213.1; -
 CC PIR: S28372; S28372.
 CC HSSP: P00725; ZCBH.
 CC InterPro: IPR000254; CBD_fungal.
 CC InterPro: IPR001547; Glyco_hydro_F5.
 CC Pfam: PF00734; CBD_1; 1.
 CC Pfam: PF00150; cellulase_1.
 CC Prodom: PD001821; CBD_fungal; 1.
 CC SMART: SM00236; tCBD; 1.
 CC

DR PROSITE: PS00562; CBD_FUNGAL; 1.
 DR PROSITE: PS00559; GLYCOSYL_HYDROL_F5; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 418 ENDOGLUCANASE EG-II.
 FT DOMAIN 22 57 CELLULOSE-BINDING (BY SIMILARITY).
 FT DOMAIN 58 91 LINKER.
 FT DOMAIN 92 418 CATALYTIC.
 FT MOD_RES 22 22 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 29 46 BY SIMILARITY.
 FT DISULFID 40 56 BY SIMILARITY.
 FT ACT_SITE 239 239 PROTON DONOR (BY SIMILARITY).
 FT ACT_SITE 350 350 NUCLEOPHILE.
 SO SEQUENCE 418 AA; 44227 MW; 264A92D552374A9B CRC64;

Query Match 7.4%; Score 93; DB 1; Length 418;
 Best Local Similarity 23.3%; Pred. No. 0.76;
 Matches 50; Conservative 21; Mismatches 72; Indels 72; Gaps 11;

QY 8 AAATFYGGDASGTMGCTGCGYGLYSTGYTNTALSTVFNDAACRSCYELRCNDGOW 67
 Db 11 AASIIYGAVAADQTVWGQC--GGIGWSGPTNCA-----PGSACSTLNPYYAQ----- 55
 QY 68 CLPGSVTATNLCPPNVALPNDGQMCNPPRHPDMAEPALQIGYRAGIVPVSRYR 127
 Db 56 CIGCATTTT-TSTRPSPGPTTTTTRATSTSSSTP-----PTS----- 90
 QY 128 PCVKKKGIRFTNGHSFNLVLTNYAG-----PGDVQSVSIRKSGSTGCMQPSRMWGOW 182
 Db 91 -----SGVFEEA-----GVNIAGDFGCTGTGTCV---TSKYVPLPKNFTG--- 127
 QY 183 OSNSTYLDGSGLSRQVAVSPDGRVTSNNVYPAQMOF 217
 Db 128 -SNNIPDGIQMOHQHEVNEDEGMTTFR---LPVGMQY 158

RESULT 10
 NA95_HUMAN STANDARD; PRT; 646 AA.
 ID NA95_HUMAN
 AC Q9UAX6; Q9UAX6; Q9NR00; Q94792;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neighbor of A-kinase anchoring protein 95 (Homologous to AKAP95
 DE protein) (HA95) (Helicase A-binding protein 95) (HA95).
 GN NAKAP95.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=20163068; PubMed=10697960;
 RA Seki N., Ueki N., Yano K., Saito T., Masuno Y., Muramatsu M.-A.;
 RT "cDNA cloning of a novel human gene NAKAP95, neighbor of A-kinase
 RT anchoring protein 95 (AKAP95) on chromosome 19p13.11-p13.12 region."; J. Hum. Genet. 45:31-37(2000).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2022332; PubMed=10761695;
 RA Orsavaik S., Elde T., Collas P., Han I.O., Taaken K., Kieff E.,
 RA Jahnson T., Skalhogg B.S.;
 RT "Identification, cloning and characterization of a novel nuclear
 RT protein, HA95, homologous to A-kinase anchoring protein 95."; Biol. Cell 92:27-37(2000).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell lymphoma, and placenta;
 RX MEDLINE=20347256; PubMed=10748171;
 RA Westberg C., Yang J.-P., Tang H., Reddy T.R., Wong-Staal F.;
 RT "A novel shuttle protein binds to RNA helicase A and activates the

retroviral constitutive transport element";
 J. Biol. Chem. 275:21396-21401(2000).
 [4]
 RP SEQUENCE OF 1-358 FROM N.A.
 RC TISSUE=Retal brain;
 RX MEDLINE=99068504; PubMed=9853615;
 RA Ueki N., Oda T., Kondo M., Yano K., Noguchi T., Muramatsu M.-A.;
 RT "Selection system for genes encoding nuclear-targeted proteins";
 RL Nat. Biotechnol. 16:1338-1342(1998).
 CC -1- FUNCTION: COULD PLAY A ROLE IN CONSTITUTIVE TRANSPORT ELEMENT
 (CTE)-MEDIATED GENE EXPRESSION. DOES NOT SEEM TO BE IMPLICATED IN
 THE BINDING OF REGULATORY SUBUNIT II OF PKA.
 CC -1- SUBUNIT: BINDS TO THE C-TERMINAL OF RNA HELICASE A.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR AT STEADY STATE BUT SHUTTLES BETWEEN
 THE NUCLEUS AND CYTOPLASM.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AB025905; BAA85003.1; -;
 DR EMBL: AJ244467; CAB65092.1; -;
 DR EMBL: AF199414; CAB65048.1; -;
 DR EMBL: AB015332; BAA34791.1; ALT_INT.
 DR InterPro: IPR000822; Znf_C2H2; 1.
 DR SMART: SM00355; Znf_C2H2; 1.
 KW Nuclear protein; Zinc-finger.
 FT DOMAIN 274 279
 FT 362 364
 FT 391 413
 FT 484 507
 FT 41 52
 FT 602 608
 FT 589 597
 FT 100 100
 FT 189 189
 FT 351 358
 FT 458 458
 FT 554 596
 FT 610 640
 FT 646 AA: 71648 MW: EED855A81BB06585 CRC64;
 SQ SEQUENCE
 Query Match 7.4%; Score 92.5; DB 1; Length 646;
 Best Local Similarity 23.6%; Pred. No. 1.3;
 Matches 60; Conservative 29; Mismatches 108; Indels 57; Gaps 13;
 2 YSSWQSAHATFYGGD-ASGTMGTCGYGNLYSTGYTNTAALSTVLFPDCAACRSCYEL- 59
 18 YSDTSAQPCDYGTWNSGTNGYGYGYGCDNTN-----YCGMATSHSHEMP 72
 60 RCDNDQWCLPBGSVYATATLCPNYALPNDGCMCPRPHPDMAEPALDQGVYRAGI 119
 73 SSOTNANTSASGSASADSV-LSRINORL-----DMVPHL---ETDMQGVYGGSG- 118
 120 VPSYRVPCVKKGIRFTI-----NGHSYFNLVLTNVAAGPDVQS-----VSIKGS 168
 119 -----GERYDYTESCDIRAVYSELDYRSQDYSELDPENMAVEGYDAYRQDFRRRGND 174
 169 T-----GW-----QPMRNACQNMQNSYLDGSLSFQVAVSDGRVTSTNNVP--- 212
 175 TFGPRAGCMARDARSGPMVAGSGRMWEDPMGARGCQMS---CASRLPSLFSQNIIPERG 231
 213 --AGMOPGOTFEFG 224
 232 MFGMRCGCAFGCG 245

RESULT 11
 CAT_MOUSE
 ID CAT_MOUSE STANDARD; PRT: 333 AA.
 AC 09R014; 09W51;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cathepsin J, a novel murine cysteine protease of the papain family
 GN CTSL OR CTSP
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=99456833; PubMed=10526153;
 RA Tislar K., Deussing J., Peters C.;
 RT "Cathepsin J, a novel murine cysteine protease of the papain family
 with a placenta-restricted expression";
 RL FEBS Lett. 459:299-304(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Placenta;
 RA Sol-Church K., French J., Troeber D., Mason R.W.;
 RT "Cloning of a mouse cysteine protease";
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Lysosomal (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 PAPAINE FAMILY OF THIOLE PROTEASES.
 CC -----
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 CC -----
 DR EMBL: AF136272; AAF13142.1; -;
 DR EMBL: AF158182; AAD41898.1; -;
 DR HSSP: P07711; ICTL.
 DR MEROPS: C01.038; -;
 DR MGD: MGI:1349426; Cstj.
 DR InterPro: IPR000668; Peptidase_C1.
 DR InterPro: IPR000169; Thiolprot_act_site.
 DR Pfam: PF00112; Peptidase_C1; 1.
 DR PRINTS: PR00705; PAPAINE.
 DR PROSITE: PS00139; THIOLE PROTEASE_CYS; 1.
 DR PROSITE: PS00639; THIOLE PROTEASE_HIS; 1.
 DR PROSITE: PS00640; THIOLE PROTEASE_ASN; 1.
 KW Hydrolyase; Thiol protease; Glycoprotein; Lysosome; Zymogen; Signal.
 FT SIGNAL 1 17
 FT PROPEP 18 112
 FT CHAIN 113 333
 FT ACT_SITE 137 137
 FT ACT_SITE 275 275
 FT ACT_SITE 299 299
 FT DISULFID 134 177
 FT DISULFID 168 210
 FT DISULFID 268 321
 FT CARBOHYD 71 71
 FT CARBOHYD 216 216
 FT CARBOHYD 220 220
 FT CARBOHYD 267 267
 FT CONFLICT 42 42
 FT CONFLICT 42 42
 SQ SEQUENCE 333 AA: 37147 MW: F9A8FPIDSA1B721 CRC64;
 Query Match 7.2%; Score 90.5; DB 1; Length 333;
 Best Local Similarity 25.0%; Pred. No. 0.98;
 Matches 57; Conservative 16; Mismatches 84; Indels 71; Gaps 14;

OY 1 DYSSW-QSAHAT-----FYGGDASGSMGTCGYNLYSGYNTAALSTVL 46
 DB 115 DYKDMREGGIVTVPARNQCKSCSNAFAAAGAIEGOMENKT--GNTPLSYONLDCSKTV 172
 OY 47 FNDGAAACRS-----CYELRCNDNDGOWCLPGSVTVTATNLCPPNYALPNDGCMCPRPRH 101
 DB 173 GNGK--COSGTAHQAFEVVLNKG-----LEAEAT-----YPEGKDG---PCRYR 213
 OY 102 FDMAE-----PAFLQIGYVRAGIVP-----SYRVPCKKKGIFFTINGH 142
 DB 214 SENASANTDYVNLPPNELYLMVAVASIGVSAIDAIDASHDFR---FYNGGIYEPNCS 269
 OY 143 SYF--NLVLTNNVAGPGDPVQSVIKSGSTGQPMRNMGMQMSNYL 188
 DB 270 SYFNHNVLYVYGSEGDV-----KDGNNYVL-IKNSGEMGMNGM 311

RESULT 12
 DPP4_HUMAN
 ID DPP4_HUMAN STANDARD; PRT; 766 AA.
 AC P27487;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dipeptidyl peptidase IV (EC 3.4.14.5) (DPP IV) (T-cell activation antigen CD26) (TP103) (Adenosine deaminase complexing protein-2) (ADABP).
 GN DPP4 OR ADCP2 OR CD26.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92329551; PubMed=1352704;
 RA Misumi Y., Hayashi Y., Arakawa F., Ikehara Y.;
 RT "Molecular cloning and sequence analysis of human dipeptidyl peptidase IV, a serine proteinase on the cell surface.";
 RL Biochim. Biophys. Acta 1131:333-336(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=95012454; PubMed=7927537;
 RA Abbott C.A., Baker E., Sutherland G.R., McCaughan G.W.;
 RT "Genomic organization, exact localization, and tissue expression of the human CD26 (dipeptidyl peptidase IV) gene.";
 RL Immunogenetics 40:331-338(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral blood;
 RX MEDLINE=92325476; PubMed=1352530;
 RA Tanaka T., Camerini D., Seed B., Torimoto Y., Dang N.H., Kameoka J., Dahlberg H.N., Schlossman S.F., Morimoto C.;
 RT "Cloning and functional expression of the T cell activation antigen CD26.";
 RL J. Immunol. 149:481-486(1992).
 RN [4]
 RP ERRATUM.
 RX MEDLINE=93171637; PubMed=8094732;
 RA Tanaka T.;
 RL J. Immunol. 150:2090-2090(1993).
 RN [5]
 RP SEQUENCE OF 1-551 FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=92165847; PubMed=1347043;
 RA Darnoul D., Lacasa M., Baricault L., Marguet D., Sapin C., Trotot P., Barbat A.;
 RT "Dipeptidyl peptidase IV (CD 26) gene expression in enterocyte-like colon cancer cell lines HT-29 and Caco-2. Cloning of the complete human coding sequence and changes of dipeptidyl peptidase IV mRNA levels during cell differentiation.";

RL J. Biol. Chem. 267:4824-4833(1992).
 RN [6]
 RP SEQUENCE OF 545-766 FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=91024044; PubMed=1977364;
 RA Darnoul D., Lacasa M., Chantrel I., Swallow D., Trugnan G.;
 RT "Isolation of a cDNA probe for the human intestinal dipeptidyl peptidase IV and assignment of the gene locus DPP4 to chromosome 2.";
 RL Ann. Hum. Genet. 54:191-197(1990).
 RN [7]
 RP SEQUENCE OF 1-31 FROM N.A.
 RX MEDLINE=96067599; PubMed=7487939;
 RA Boehn S.K., Gum J.R., Jr., Erickson R.H., Hicks J.W., Kim Y.S.;
 RT "Human dipeptidyl peptidase IV gene promoter: tissue-specific regulation from a TATA-less GC-rich sequence characteristic of a housekeeping gene promoter.";
 RL Biochem. J. 311:835-843(1995).
 RN [8]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=93210468; PubMed=8096237;
 RA Moritson M.E., Vijayasatradhi S., Engelstein D., Albino A.P., Houghton A.N.;
 RT "A marker for neoplastic progression of human melanocytes is a cell surface ectopeptidase.";
 RL J. Exp. Med. 177:1135-1143(1993).
 CC -1- FUNCTION: REMOVES N-TERMINAL DIPEPTIDES SEQUENTIALLY FROM POLYPEPTIDES HAVING UNSUBSTITUTED N-TERMINI PROVIDED THAT THE PENULTIMATE RESIDUE IS PROLINE. PLAYS A ROLE IN T CELL ACTIVATION.
 CC -1- CATALYTIC ACTIVITY: DIPEPTIDYL-POLYPEPTIDE + H(2)O = DIPEPTIDE + POLYPEPTIDE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS IN A SOLUBLE FORM.
 CC -1- PTM: THE SOLUBLE FORM (SDPP) DERIVES FROM THE MEMBRANE FORM (MDPP) BY PROTEOLYTIC PROCESSING.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLYL OLIGOPEPTIDASE FAMILY.
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD26 entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd26.htm".
 CC -----
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 CC -----
 DR EMBL: U13735; AAB60646.1; -
 DR EMBL: U13710; AAB60646.1; JOINED.
 DR EMBL: U13711; AAB60646.1; JOINED.
 DR EMBL: U13712; AAB60646.1; JOINED.
 DR EMBL: U13713; AAB60646.1; JOINED.
 DR EMBL: U13714; AAB60646.1; JOINED.
 DR EMBL: U13715; AAB60646.1; JOINED.
 DR EMBL: U13716; AAB60646.1; JOINED.
 DR EMBL: U13717; AAB60646.1; JOINED.
 DR EMBL: U13718; AAB60646.1; JOINED.
 DR EMBL: U13719; AAB60646.1; JOINED.
 DR EMBL: U13720; AAB60646.1; JOINED.
 DR EMBL: U13721; AAB60646.1; JOINED.
 DR EMBL: U13722; AAB60646.1; JOINED.
 DR EMBL: U13723; AAB60646.1; JOINED.
 DR EMBL: U13724; AAB60646.1; JOINED.
 DR EMBL: U13725; AAB60646.1; JOINED.
 DR EMBL: U13726; AAB60646.1; JOINED.
 DR EMBL: U13727; AAB60646.1; JOINED.
 DR EMBL: U13728; AAB60646.1; JOINED.
 DR EMBL: U13729; AAB60646.1; JOINED.
 DR EMBL: U13730; AAB60646.1; JOINED.
 DR EMBL: U13731; AAB60646.1; JOINED.

DR EMBL: U13732; AAB60646.1; JOINED.
 DR EMBL: U13733; AAB60646.1; JOINED.
 DR EMBL: U13734; AAB60646.1; JOINED.
 DR EMBL: M74777; AAA51943.1; -
 DR EMBL: M80536; AAA52308.1; -
 DR EMBL: X60708; CAA43118.1; -
 DR EMBL: S79876; AAB35614.1; -
 DR PIR: S24313; CDH026.
 DR MEMOPS: S09.003; -
 DR MIM: 102720; -
 DR InterPro: IPR002469; DPPV_N_term.
 DR InterPro: IPR000379; Est_Hlp_ChoEstactsite.
 DR InterPro: IPR001375; Peptidase_S9.
 DR InterPro: IPR002471; Prol_endopep_ser.
 DR Pfam: PF00930; DPPV_N_term; 1.
 DR Pfam: PF00326; Peptidase_S9; 1.
 DR ProSite: PS00708; PRO_ENDOPEP_SER; 1.
 DR HydroLase: AminoPeptidase; Dipeptidase; Serine protease;
 KW Transmembrane; Glycoprotein; Signal-anchor;
 FT CHAIN 1 766
 FT CHAIN 39 766
 FT DOMAIN 1 6
 FT TRANSMEM 7 28
 FT DOMAIN 29 766
 FT ACT_SITE 630 630
 FT ACT_SITE 708 708
 FT ACT_SITE 740 740
 FT CARBOHYD 85 85
 FT CARBOHYD 92 92
 FT CARBOHYD 150 150
 FT CARBOHYD 219 219
 FT CARBOHYD 229 229
 FT CARBOHYD 281 281
 FT CARBOHYD 321 321
 FT CARBOHYD 520 520
 FT CARBOHYD 685 685
 FT CONFLICT 6 6
 FT CONFLICT 7 7
 FT CONFLICT 437 437
 FT CONFLICT 557 557
 FT CONFLICT 663 663
 FT SEQUENCE 766 AA: 88278 MW: 5FBA2C662D6117 CRC64;
 Query Match 6.9%; Score 87; DB 1; Length 766;
 Best Local Similarity 24.2%; Pred. No. 4.7;
 Matches 48; Conservative 20; Mismatches 66; Indels 64; Gaps 11;
 QY 12 FYGGGDSAGTGTGCGYGNLYS---TGVTNTAALS-----TVLFNDGACRSCY 57
 DB 416 YVLSNEKYGKGR---NLKRIQLSDYTKVCLSCGLNPERCQYYSFSKEA---KYY 468
 QY 58 ELRGDNG--QMLPGSYVYATNLCPNYALP-----NDGCGWGN- 96
 DB 469 QLRSGRLPLVLYLHSSVADKGLRVLEDSALDKMLQNVQMPKSLDFITLNETKFEVQM 528
 QY 97 --PPRHFMADEPAFLQGVYRAGIVPVSYRRVPCVKKCGICFTINGSYFELVLTNVA 154
 DB 529 ILP--PHFQSKKYPILLLOY-AG-----PCSKADIVYFLNMAVY-----LA 568
 QY 155 GRPDVQSVSLKSGSYGQ 172
 DB 569 STEKITVASFDGSGCYQ 586
 RESULT 13
 YMV2.CABEL
 ID YMV2.CABEL STANDARD; PRT; 1246 AA.
 AC P34504; P34505; P34506; P90907;
 DT 01-FEB-1994 (rel. 28, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DT 01-MAR-2002 (rel. 41, Last annotation update)
 DE Hypothetical 130.6 kDa protein K04H4.2 in chromosome III.

GN K04H4.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RC MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kistler J., Lister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Sims M., Smaildon N., Smith A., Smith M., Sonnenhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterson R., Watson A., Wellstock L., Wilkinson-Sproat J.,
 RA Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RN Nature 368:32-38(1994).
 RP [2]
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: K04H4.2A (SHOWN HERE) AND
 CC K04H4.2B; ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: TO CHITIN-BINDING MOTIFS.
 CC -----
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 CC -----
 DR EMBL: Z27078; CAA81587.1; -
 DR EMBL: Z27078; CAA81588.1; -
 DR PIR: S40992; S40992.
 DR PIR: S40993; S40993.
 DR PIR: S40994; S40994.
 DR HSP: P10968; 2CWG.
 DR WormPep: K04H4.2A; CE19967.
 DR WormPep: K04H4.2B; CE19968.
 DR InterPro: IPR002557; Chitin_binding.
 DR InterPro: IPR002899; EB.
 DR SMART: SM00494; ChIBD2; 1.
 DR SMART: SM00289; WRI; 14.
 KW Hypothetical protein; Alternative splicing.
 FT VARSPLIC 166 529
 FT TTPPTPTPTPKKLCSSNTDEVNSLGGASSSSNATGCGYN
 FT ANCTSDDECPPTFKCYGCGCCCLAVCPRLATLVKFTCKTOYI
 FT CRANHECFEGGCGPTLILAVIKSOVLTKDNENHETK
 FT LIIGCEVDTRVKKCDIILPEMSECEVDCGCGOPKARC
 FT GNGMALSLPVHCSLSDCPILASRCCEVCGCPPISESADST
 FT SDVSEETPVITKEIETATKRVKKKDKKISGVSTINKKL
 FT STQRCDLHTLPDPDTGLSGKCCCKLNKHCNCPGIVPTISQ
 FT SASNHDICPSSSKCTLLNKEHFAVCYSPGLVGVCSVAVY
 FT SSECPIGSEVDFRGTSRCRYSLCCPSYPCNGRQ -> Q
 FT (IN ISOFORM K04H4.2B).
 FT DSDTSTNTPSPQETTTTKTKKSSSKKHRRKKKDDVP
 FT LSDPLNDPFIQPGCYGCPRLSLNDEVLIRADGDECTA
 FT GLHCPATNLCCPILPLTDPKRNPKKRTKRRKQKODGEM
 FT EASANFPDSDARFSYSYSGCGWG -> VG (IN
 FT ISOFORM K04H4.2B).
 FT SEQUENCE 1246 AA: 130610 MW: 4FA1A17D3F9606C4 CRC64;
 Query Match 6.9%; Score 86.5; DB 1; Length 1246;
 Best Local Similarity 23.3%; Pred. No. 8.8;
 Matches 50; Conservative 16; Mismatches 82; Indels 67; Gaps 9;

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OY 18 ASGTMGCTCGYGNLYSTGYNTALSTVLPNDGA-ACRSCYELRCNDG-----QMCL 69
DB 824 AGGCVNCGCGGYTCGSMGLCCAGTSTVTKCLDSDAAGACIP-SCIGDGGCGVQVSYTG 882
OY 70 PGSVYVATNLCPPNYALPNDGCGMCPRPHEDEMAEPALQIGYVRAGIVPISRYRVC 129
DB 883 SG-YTCTTGNIICPILNSCPN--GSEV-----LGPRTINGLCPRTGY----- 918
OY 130 VKKGIRPTINGHSYFNVLVTNVAAGPDQVSINSGSTGWMQMSNNQNMQNSYLD 189
DB 919 -----TYOONLCCSAYCTDGTGLPSVNGVCT-----D 946
OY 190 GOSLFOYAVSDGRTVTSNNVYPAGMOFGQTEEG 224
DB 947 GYSLINGVCCP--ASYTCTDELSTGPGCTGFENG 979

RESULT 14
FLAL_CAMJE STANDARD; PRT: 571 AA.
ID P56963: Q9PMQ0:
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellin A.
GN FLA OR CJI339C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCTC 11168;
RA PARKHILL J., Wren B.W., Mungall K., Kelley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,
RA Jagsels K., Karyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RU Nature 403:665-668(2000).
CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC -1- FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -1- SUBUNIT: HETEROPOLYMER OF FLA AND FLAB.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DB EMBL: AL139078: CAB73766.1;
DB InterPro: IPR001028: Flagellin_C.
DB InterPro: IPR001492: Flagellin_N.
DB PRINTS: PR00207: FLAGELLIN.
DB ProDom: PD000316: Flagellin_C; 1.
DB KEGG: Complete proteome.
DB INIT MET 0 BY SIMILARITY.
SO SEQUENCE 571 AA; 58907 MW; 9C6B3B2A10C1AE863 CRC64;

Query Match 6.8%; Score 85; DB 1; Length 571;
Best Local Similarity 23.4%; Pred. No. 5.1;
Matches 51; Conservative 26; Mismatches 71; Indels 70; Gaps 10;
OY 2 YSSWQSAHATPYGGDASGTCGTCGYGNLYSTGYNTAA-----LSTVL-----FN 48
DB 393 YSS-YSATWSSAGSGFSSGS-GYVSGSKKNSTGFANALISAASQLSTVYNNVSAGSGFS 450
OY 49 DGAAC-----RSCYELRCNDGQWCLPGSVYVATNLCPPNYALPNDGCGMCPRP 101

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DB 451 SGSTLSGEAFATKTTAFGVKDEFAVTTLKGAAMV----- 484
OY 102 FDMAPAFLOIGYVRAGIVPISRYRVCVKKGIRPTINGHSYFNVLVTNV---AGPD 158
DB 485 MDIAETALTNDQIRADI-----GSVQNVY--STINNITVQVWVAESQ 529
OY 159 VQVSIRKSSGTGQPMRNMQNMQNSYLDGSLSPQ 196
DB 530 IRVDVFAESANYSKAN---TLAQSGSYMAQAQANSQ 563

RESULT 15
CICB_BACTG STANDARD; PRT: 1176 AA.
ID CICB_BACTG
AC P56953:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cryIcb (Insecticidal delta-endotoxin
DE CryIc(b)) (Crystalline entomocidal protoxin) (133 kDa crystal protein).
GN CRYICB OR CRYIC(B).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=HD-29;
RX MEDLINE=93236401; PubMed=8476286;
RA Kalman S.S.;
RT "Cloning a novel cryIc-type gene from a strain of Bacillus
RT thuringiensis galleriae."
RT Appl. Environ. Microbiol. 59:1131-1137(1993).
CC -1- FUNCTION: PROMOTES COLICIDEMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS. TOXIC TO SPOOPTERA EXIGUA AND
CC TRICHOPLUSTIA NI.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DB EMBL: M97880; ; NOT_ANNOTATED_CDS.
DB HSSP: P02965; ICIV.
DB InterPro: IPR001178: Endotoxin.
DB Pfam: PF00555; endotoxin; 1.
DB Toxin: Sporulation.
DB KEGG: 1176 AA; 132867 MW; 108233494C2AC018 CRC64;
SO SEQUENCE 1176 AA; 108233494C2AC018 CRC64;

Query Match 6.7%; Score 84.5; DB 1; Length 1176;
Best Local Similarity 22.5%; Pred. No. 12;
Matches 66; Conservative 30; Mismatches 98; Indels 99; Gaps 17;
OY 2 YSSWQSAHATPYGGD--ASGTMGCTCGYGNLYSTG---TNTAALSTVLPNDGACRSC 56
DB 310 FTDWFSVGRNFYWGHRVYSNRIGG---GNITSPITGRANQDEPRSPFEN-GVFRRL 361
OY 57 -----YELRCNDGQWCLP-GSVYVATNLCPPNYALPNDGCGMCPRP 99
DB 365 SNPTFRPLQGWPPAPFNLKRVGEVERSTPLNSTYGRGTVDSTLPEPDMS--VPPR 422
OY 100 PHFD--MAEPALQIGYVRAG-----IVPISRYRVCVK----- 131

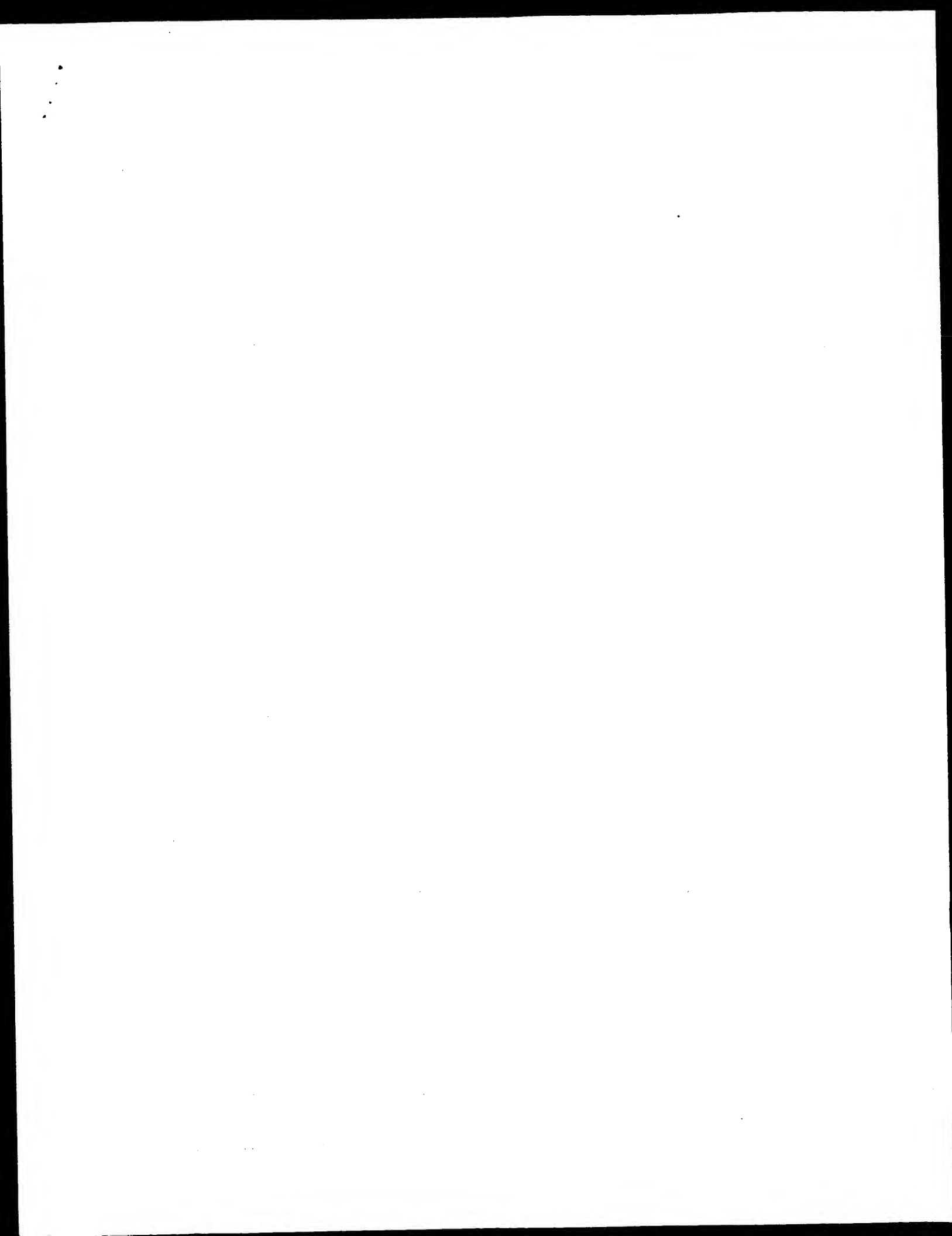
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Db 423 EGYSHRLCHATEVO---RSGTPELTTCPVFSWTHRSATDRNIYPDVINQIPLVKAENL 478
OY 132 -----KG--IRETINGH-----SYENLVL-----VTNAGPBGDVOSVSIK 165
Db 479 TSGTSVVRGPGFTGDIIRTNVNGSVLSMSLNFSTTLORYRVRVRYAASQTMVMSVTVG 538
OY 166 GSSTGMOPMSRNGQNMWQNSYLDGOSLSF-----QVAVSDGRTVT-SNNV 210
Db 539 GSTTG-----NCGFPSTMSANGALTSQSPRFAEPYGISASGASISISNNV 587

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Search completed: October 11, 2002, 14:57:35
 Job time : 7.83764 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:54:05 ; Search time 8.83985 Seconds
(without alignments)
624,466 Million cell updates/sec

Title: US-09-896-301-6
Sequence: 1 DYSSWQSAHATFYGGDASG.....SNNVDPAGMFGOTFGGQF 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5a_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5b_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6a_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6b_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1257	100.0	226	2	US-08-440-517A-6
2	1257	100.0	226	4	US-09-092-160-6
3	1021.5	81.3	227	4	US-09-092-160-7
4	959.5	76.3	228	4	US-08-440-517A-2
5	863.5	68.7	225	2	US-08-440-517A-5
6	863.5	68.7	225	2	US-08-440-517A-5
7	863.5	68.7	225	2	US-08-440-517A-5
8	791.5	63.0	222	2	US-08-845-539-2
9	787	62.6	222	2	US-08-440-517A-3
10	787	62.6	222	4	US-09-092-160-3
11	783.5	62.3	222	4	US-09-362-642-2
12	742	59.0	227	2	US-08-440-517A-4
13	742	59.0	227	2	US-08-440-517A-4
14	726.5	57.8	179	4	US-08-845-539-6
15	726.5	57.8	179	4	US-08-845-539-6
16	682.5	54.3	167	2	US-08-845-539-4
17	682.5	54.3	167	4	US-09-362-642-4
18	251.5	20.0	261	1	US-07-971-096-2
19	251.5	20.0	261	1	US-08-175-096-2
20	225	17.9	246	4	US-08-441-507-21
21	219	17.4	272	4	US-08-441-507-15
22	213.5	17.0	263	1	US-07-971-096-4
23	213.5	17.0	263	4	US-08-413-974-6
24	213.5	17.0	263	4	US-08-413-974-6
25	213.5	17.0	263	4	US-08-433-418-6
26	213.5	17.0	263	4	US-08-433-288-6
27	213.5	17.0	263	4	US-08-174-739A-6

28	202	16.1	245	4	US-08-441-507-24	Sequence 24, App1
29	169	13.4	200	4	US-08-441-507-4	Sequence 4, App1
30	168	13.4	197	4	US-08-441-507-5	Sequence 5, App1
31	125.5	10.0	122	4	US-08-441-507-23	Sequence 23, App1
32	109.5	8.7	145	4	US-08-413-974-4	Sequence 4, App1
33	109.5	8.7	145	4	US-08-434-418-4	Sequence 4, App1
34	109.5	8.7	145	4	US-08-433-288-4	Sequence 4, App1
35	109.5	8.7	145	4	US-08-174-739A-4	Sequence 4, App1
36	107.5	8.6	145	4	US-08-441-507-2	Sequence 2, App1
37	106.5	8.5	145	4	US-08-441-507-16	Sequence 16, App1
38	102	8.1	138	4	US-08-144-121-3	Sequence 3, App1
39	89	7.1	1147	1	US-08-144-121-3	Sequence 3, App1
40	89	7.1	1147	2	US-08-735-893-3	Sequence 3, App1
41	89	7.1	1165	1	US-08-144-121-2	Sequence 2, App1
42	89	7.1	1165	2	US-08-735-893-3	Sequence 2, App1
43	87	6.9	593	5	PCT-US93-07923-11	Sequence 11, App1
44	87	6.9	755	5	PCT-US93-07923-3	Sequence 3, App1
45	87	6.9	759	5	PCT-US93-07923-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-08-440-517A-6

Sequence 6, Application US/08440517A
Patent No. 5959082

GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SCHERBAN, TATYANA;
APPLICANT: SHI, JUN

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESS: INTELLECTUAL PROPERTY OFFICE, THE
ADDRESS: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 226
TYPE: AMINO ACID
TOPOLOGY: UNKNOWN

US-08-440-517A-6

Query Match 100.0%; Score 1257; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 6,7e-112;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DYSSWQSAHATFYGGDASGTCGYNLVSTGYNTAALSTVLPNDGAACRCYEIR	60
DB	1	DYSSWQSAHATFYGGDASGTCGYNLVSTGYNTAALSTVLPNDGAACRCYEIR	60
QY	61	CDNDGQMCLEGSVTATNLCPNTALPNDGQMCNPPRPHDMAEPFLQIGYVRACTV	120
DB	61	CDNDGQMCLEGSVTATNLCPNTALPNDGQMCNPPRPHDMAEPFLQIGYVRACTV	120
QY	121	PVSRYRVCYKKGIRFTNGHSYFLVYTVNAPRGVQSVSTIGSSTGQWPSRMNQ	180
DB	121	PVSRYRVCYKKGIRFTNGHSYFLVYTVNAPRGVQSVSTIGSSTGQWPSRMNQ	180

QY 181 NMOSNSYLDGOSLSFOVAVSDGRTVTSNNVVPAGMOFGQTEGGOF 226
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 NMOSNSYLDGOSLSFOVAVSDGRTVTSNNVVPAGMOFGQTEGGOF 226

RESULT 2 US-09-092-160-6

; Sequence 6, Application US/09092160C
 ; Patent No. 6255466
 ; GENERAL INFORMATION:
 ; APPLICANT: Cosgrove, Daniel J
 ; APPLICANT: McQueen-Mason, Simon
 ; APPLICANT: Guillinan, Mark J
 ; APPLICANT: Shcherban, Tatyana
 ; APPLICANT: Shi, Jun
 ; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 ; FILE REFERENCE: 1194/JC114US3
 ; CURRENT APPLICATION NUMBER: US/09/092,160C
 ; CURRENT FILING DATE: 1998-06-05
 ; EARLIER APPLICATION NUMBER: 08/440,517
 ; EARLIER FILING DATE: 1995-05-12
 ; EARLIER APPLICATION NUMBER: 08/242,090
 ; EARLIER FILING DATE: 1994-05-12
 ; EARLIER APPLICATION NUMBER: 08/060,944
 ; EARLIER FILING DATE: 1993-05-12
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
 ; OTHER INFORMATION: expansin
 US-09-092-160-6

Query Match 100.0%; Score 1257; DB 4; Length 226;
 Best Local Similarity 100.0%; Pred. No. 6.7e-112;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSWOSAHATFYGGDASGTMGTCGYGNLYSTGYTNTALSTVLFNDGAACRSCYEL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 DYSWOSAHATFYGGDASGTMGTCGYGNLYSTGYTNTALSTVLFNDGAACRSCYEL 60
 QY 61 CDNDGQWCLPGSVYVATNLCPPNYALPNDGQWCPNPPHFDMAEPALQIGVYRAGI 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 CDNDGQWCLPGSVYVATNLCPPNYALPNDGQWCPNPPHFDMAEPALQIGVYRAGI 120
 QY 121 PVSYRRVPCYKKGIRFTINGHSYFNLYVTNAGPGDVQSVSIKGSSTGQPMSSRNMG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 PVSYRRVPCYKKGIRFTINGHSYFNLYVTNAGPGDVQSVSIKGSSTGQPMSSRNMG 180
 QY 181 NMOSNSYLDGOSLSFOVAVSDGRTVTSNNVVPAGMOFGQTEGGOF 226
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 NMOSNSYLDGOSLSFOVAVSDGRTVTSNNVVPAGMOFGQTEGGOF 226

RESULT 3
 US-09-092-160-7
 ; Sequence 7, Application US/09092160C
 ; Patent No. 6255466
 ; GENERAL INFORMATION:
 ; APPLICANT: Cosgrove, Daniel J
 ; APPLICANT: McQueen-Mason, Simon
 ; APPLICANT: Guillinan, Mark J
 ; APPLICANT: Shcherban, Tatyana
 ; APPLICANT: Shi, Jun
 ; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 ; FILE REFERENCE: 1194/JC114US3
 ; CURRENT APPLICATION NUMBER: US/09/092,160C
 ; CURRENT FILING DATE: 1998-06-05
 ; EARLIER APPLICATION NUMBER: 08/440,517

; EARLIER FILING DATE: 1995-05-12
 ; EARLIER APPLICATION NUMBER: 08/242,090
 ; EARLIER FILING DATE: 1994-05-12
 ; EARLIER APPLICATION NUMBER: 08/060,944
 ; EARLIER FILING DATE: 1993-05-12
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: cucumber
 ; OTHER INFORMATION: expansin
 US-09-092-160-7

Query Match 81.3%; Score 1021.5; DB 4; Length 227;
 Best Local Similarity 78.0%; Pred. No. 1.5e-89;
 Matches 177; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

QY 1 DYSWOSAHATFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 59
 ||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 DYSWOSAHATFYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 60
 QY 60 RCDNDGQWCLPGSVYVATNLCPPNYALPNDGQWCPNPPHFDMAEPALQIGVYRAGI 119
 ||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 TCTNDPKWCLPGIRVYATNLCPPNYALPNDGQWCPNPPHFDMAEPALQIGVYRAGI 120
 QY 120 PVSYRRVPCYKKGIRFTINGHSYFNLYVTNAGPGDVQSVSIKGSSTGQPMSSRNMG 179
 ||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 PVSYRRVPCYKKGIRFTINGHSYFNLYVTNAGPGDVQSVSIKGSSTGQPMSSRNMG 180
 QY 180 NMOSNSYLDGOSLSFOVAVSDGRTVTSNNVVPAGMOFGQTEGGOF 226
 ||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 NMOSNSYLDGOSLSFOVAVSDGRTVTSNNVVPAGMOFGQTEGGOF 227

RESULT 4

US-08-440-517A-2
 ; Sequence 2, Application US/08440517A
 ; Patent No. 5959082
 ; GENERAL INFORMATION:
 ; APPLICANT: COSGROVE, DANIEL J.;
 ; APPLICANT: GUILLINAN, MARK;
 ; APPLICANT: SCHERBAN, TATYANA;
 ; APPLICANT: SHI, JUN
 ; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
 ; ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
 ; STREET: 113 TECHNOLOGY CENTER
 ; CITY: UNIVERSITY PARK
 ; STATE: PENNSYLVANIA
 ; COUNTRY: UNITED STATES OF AMERICA
 ; ZIP: 16802-7000
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: NEC 286
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/440,517A
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 228
 ; TYPE: AMINO ACID
 ; TOPOLOGY: UNKNOWN
 US-08-440-517A-2

Query Match 76.3%; Score 959.5; DB 2; Length 228;

Best Local Similarity 75.0%; Pred. No. 1,2e-83;
Matches 165; Conservative 23; Mismatches 31; Indels 1; Gaps 1;

QY 5 WQSAHATFYGGDASGTGCTGCGNLSTGY-TNTALSTVLFNDGAACRSCELRCDN 63
1 :|||||
Db 5 WYNAHATFYGGDASGTGACGYNLYSQGYGTNTALSTALFNNGLSGCACFEIRCON 64
64 DQOMCLPGSVTVATNLCPPNYALPNDGMCNPPRPHDMAEPFLQIGYRAGIYVYS 123
65 DQKMCPLPGSVTVATNFCPPNALLNMGKCNPPQOIFDLSQPVFORIAQYRAGIYVVA 124
QY 124 YRRVPCVKKGIRFTINGHSYFNLYVTNVAGPDVQSVYSIKSGSTGQPMRMMGQNMQ 183
125 YRRVPCVKKGIRFTINGHSYFNLYVTNVAGPDVQSVYSIKSGSTGQPMRMMGQNMQ 184
QY 184 SNSYLDGSLSFQVAVSDGRTVTSNNVYPAGMGQTFEG 223
185 SNSYLDGSLSFQVAVSDGRTVTSNNVYPAGMGQTFEG 224

RESULT 5

US-09-092-160-2
Sequence 2, Application US/09092160C
Patent No. 6255466

GENERAL INFORMATION:

APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guillinan, Mark J
APPLICANT: Shepherdan, Tatyana
APPLICANT: Shi, Jun

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

FILE REFERENCE: 1194/1C114053

CURRENT APPLICATION NUMBER: US/09/092,160C

EARLIER FILING DATE: 1998-06-05

EARLIER APPLICATION NUMBER: 08/440,517

EARLIER FILING DATE: 1995-05-12

EARLIER APPLICATION NUMBER: 08/242,090

EARLIER FILING DATE: 1994-05-12

EARLIER APPLICATION NUMBER: 08/060,944

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 228

TYPE: PR

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: UNSURE

LOCATION: 211

OTHER INFORMATION: Xaa is unknown or other.

Query Match 76.3%; Score 959.5; DB 4; Length 228;
Best Local Similarity 75.0%; Pred. No. 1,2e-83;

Matches 165; Conservative 23; Mismatches 31; Indels 1; Gaps 1;

QY 5 WQSAHATFYGGDASGTGCTGCGNLSTGY-TNTALSTVLFNDGAACRSCELRCDN 63
1 :|||||
Db 5 WYNAHATFYGGDASGTGACGYNLYSQGYGTNTALSTALFNNGLSGCACFEIRCON 64
64 DQOMCLPGSVTVATNLCPPNYALPNDGMCNPPRPHDMAEPFLQIGYRAGIYVYS 123
65 DQKMCPLPGSVTVATNFCPPNALLNMGKCNPPQOIFDLSQPVFORIAQYRAGIYVVA 124
QY 124 YRRVPCVKKGIRFTINGHSYFNLYVTNVAGPDVQSVYSIKSGSTGQPMRMMGQNMQ 183
125 YRRVPCVKKGIRFTINGHSYFNLYVTNVAGPDVQSVYSIKSGSTGQPMRMMGQNMQ 184
QY 184 SNSYLDGSLSFQVAVSDGRTVTSNNVYPAGMGQTFEG 223
185 SNSYLDGSLSFQVAVSDGRTVTSNNVYPAGMGQTFEG 224

RESULT 6

US-08-440-517A-5
Sequence 5, Application US/08440517A
Patent No. 5959082

GENERAL INFORMATION:

APPLICANT: COSGROVE, DANIEL J.;

APPLICANT: GUILLINAN, MARK;

APPLICANT: SHEPHERDAN, TATYANA;

APPLICANT: SHI, JUN

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE

ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY

STREET: 113 TECHNOLOGY CENTER

CITY: UNIVERSITY PARK

STATE: PENNSYLVANIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 16802-7000

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: NEC 286

OPERATING SYSTEM: DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,517A

FILING DATE:

CLASSIFICATION: 530

INFORMATION FOR SEQ ID NO: 5

SEQUENCE CHARACTERISTICS:

LENGTH: 225

TYPE: AMINO ACID

TOPOLOGY: UNKNOWN

US-08-440-517A-5

Query Match 68.7%; Score 863.5; DB 2; Length 225;
Best Local Similarity 69.3%; Pred. No. 1,5e-74;

Matches 158; Conservative 24; Mismatches 41; Indels 5; Gaps 4;

QY 1 DYSSQSAHATFYGGDASGTGCTGCGNLSTGY-TNTALSTVLFNDGAACRSCELRCDN 59
1 :|||||
Db 1 DNGMGRGHATFYGGDASGTGACGYNLYSQGYGTNTALSTALFNNGLSGCACFEIRCON 60
60 RCDNDGOMCLPGSVTVATNLCPPNYALPNDGMCNPPRPHDMAEPFLQIGYRAGI 119
61 TCEDDPEMCLPGSVTVATNLCPPNYALPNDGMCNPPRPHDMAEPFLQIGYRAGI 117
QY 120 VPRVPCVKKGIRFTINGHSYFNLYVTNVAGPDVQSVYSIKSGSTG-WQPMRMM 178
121 VPRVPCVKKGIRFTINGHSYFNLYVTNVAGPDVQSVYSIKSGSTG-WQPMRMM 177
Db 118 VPRVPCVKKGIRFTINGHSYFNLYVTNVAGPDVQSVYSIKSGSTG-WQPMRMM 178
119 VPRVPCVKKGIRFTINGHSYFNLYVTNVAGPDVQSVYSIKSGSTG-WQPMRMM 177
QY 179 GONNOSNYLDGSLSFQVAVSDGRTVTSNNVYPAGMGQTFEG 226
180 GONNOSNYLDGSLSFQVAVSDGRTVTSNNVYPAGMGQTFEG 225
Db 178 GONNOSNYLDGSLSFQVAVSDGRTVTSNNVYPAGMGQTFEG 225

RESULT 7

US-09-092-160-5
Sequence 5, Application US/09092160C
Patent No. 6255466

GENERAL INFORMATION:

APPLICANT: Cosgrove, Daniel J

APPLICANT: McQueen-Mason, Simon

APPLICANT: Guillinan, Mark J

APPLICANT: Shepherdan, Tatyana

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

FILE REFERENCE: 1194/1C114053

CURRENT APPLICATION NUMBER: US/09/092,160C

CURRENT FILING DATE: 1998-06-05

EARLIER APPLICATION NUMBER: 08/440,517

QY 123 SYRVPVCKKGGIRFTINGSHYFNLVLTNVAGPDVQSVISKSGSTGQPMRNMGMW 182
DB 117 MYRVRCKRSGIRFTINGSHYFNLVLTNVAGDVSVMKSRKMKWLMNRNMGMW 176
QY 183 QSNSTLQGSLSFOVAASDGRVTSMNVVPGMFGQTFEGGOF 226
DB 177 QSNSTLQGSLSFVVTTSDRSRVSVFNAPPTWSFGQTYTGOF 220

RESULT 10

US-09-092-160-3
Sequence 3, Application US/09092160C
Patent No. 6255466
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Gullitnan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 222
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: rice expansin
NAME/KEY: UNSURE
LOCATION: (14)..(58)
OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160-3

Query Match 62.6%; Score 787; DB 4; Length 222;

Best Local Similarity 65.2%; Pred. No. 2,8e-67;

Matches 146; Conservative 21; Mismatches 47; Indels 10; Gaps 3;

QY 5 WQSHATFYGGDASGTGTCGYNLYSTGY-TNTAALSTVLPNDGACRSCYELKCDN 63
DB 5 WINHATFYXXGDXXTMGACGGLYSQYGLTALSTALFDGLSCGACXELKCVN 64
QY 64 DQWCLPG-SVTVATNLCPNYALPNDGCMCPRPHEFDMAPFLQIGVYRAGTIPV 122
DB 65 DPQWICIGRISIVTATNFCPP-----GGACDPRNHNDLSQPIYKALKSGTIPV 116
QY 123 SYRVPVCKKGGIRFTINGSHYFNLVLTNVAGPDVQSVISKSGSTGQPMRNMGMW 182
DB 117 MYRVRCKRSGIRFTINGSHYFNLVLTNVAGDVSVMKSRKMKWLMNRNMGMW 176
QY 183 QSNSTLQGSLSFOVAASDGRVTSMNVVPGMFGQTFEGGOF 226
DB 177 QSNSTLQGSLSFVVTTSDRSRVSVFNAPPTWSFGQTYTGOF 220

RESULT 11

US-09-362-642-2
Sequence 2, Application US/09362642
Patent No. 6350935
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes

FILE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 225
TYPE: PRT
ORGANISM: Lycopersicon esculentum cv. 75
US-09-362-642-2

Query Match 62.3%; Score 783.5; DB 4; Length 225;

Best Local Similarity 70.6%; Pred. No. 6.1e-67;

Matches 137; Conservative 24; Mismatches 28; Indels 5; Gaps 3;

QY 4 SMOHATFYGGDASGTGTCGYNLYSTGY-TNTAALSTVLPNDGACRSCYELKCDN 62
DB 32 SWEHATFYGGDASGTGTCGYNLYSOGYGVNTALSTALFNNGLSCGACFELKCT 91
QY 63 N--DQWCLPG--SVTVATNLCPNYALPNDGCMCPRPHEFDMAPFLQIGVYRAG 118
DB 92 NTPWKMCLPGNPSILITATNFCPPNYALPNDGCMCPRPHEFDMAPFLKLAQYRAG 151
QY 119 IVPVSRVPVCKKGGIRFTINGSHYFNLVLTNVAGPDVQSVISKSGSTGQPMRNMW 178
DB 152 IYVYTRIRPCRKGGIRFTINGSHYFNLVLTNVAGDGIKWKVGGTKTNMIALSRW 211
QY 179 GQWQSNSTLQGS 192
DB 212 GQWQSNSTLQGS 225

RESULT 12

US-08-440-517A-4

Sequence 4, Application US/08440517A

Patent No. 5959082

GENERAL INFORMATION:

APPLICANT: COSGROVE, DANIEL J.;

APPLICANT: GULLITNAN, MARK;

APPLICANT: SCHERBAN, TATYANA;

APPLICANT: SHI, JUN

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE

STREET: 113 TECHNOLOGY CENTER

CITY: UNIVERSITY PARK

STATE: PENNSYLVANIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 16802-7000

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: NEC 286

OPERATING SYSTEM: DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA: 5.17A

APPLICATION NUMBER: US/08/440,517A

FILING DATE:

CLASSIFICATION: 530

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 227

TYPE: AMINO ACID

TOPOLOGY: UNKNOWN

US-08-440-517A-4

Query Match 59.0%; Score 742; DB 2; Length 227;

Best Local Similarity 64.0%; Pred. No. 5.4e-63;

Matches 137; Conservative 24; Mismatches 49; Indels 4; Gaps 3;

QY 6 QSHATFYGGDASGTGTCGYNLYSTGY-TNTAALSTVLPNDGACRSCYELKCD-N 63

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Db 6 QSAFAFYGGKDGSCMTGACGCGNLYNAGYGLYNALSSALFNDGAMCGACTTTCDS 65
QY 64 DGQWCLPG--SVYATATNLCPPNVALPNDGWCNPPRPFMDAEPALQIGYRAGIYP 121
Db 66 QTKWCKRPGGNSLITITATNLCXPMWALPNSGWCNPLKHFDMQSPAMENIAVYQAGIYP 125
QY 122 VSYRRVPCVKKGGIRFTINGSHSYFNLYLVTVNAGPDVQSVISKSSITGMQPSRMNGON 181
Db 126 VNKRYVPXKRGSGIRFPAISGHDYFELVTVTVNAGSGVAVQMSIKGSNTGMAMSRMNGAN 185
QY 182 WQSNAYLDGQSLSEFOYVAVSDGRFTVTSNNVYPAGM 215
Db 186 WQSNAYLAGQSLSFIVQDDGRKVTAMNAPAXM 219
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RESULT 13
US-09-092-160-4
; Sequence 4, Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Guillian, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C1140S3
; CURRENT APPLICATION NUMBER: US/09/092,160C
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 08/440,517
; EARLIER FILING DATE: 1995-05-12
; EARLIER APPLICATION NUMBER: 08/242,090
; EARLIER FILING DATE: 1994-05-12
; EARLIER APPLICATION NUMBER: 08/060,944
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
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LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
; OTHER INFORMATION: expansin
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (2)-(227)
; OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160-4
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Query Match 59.0%; Score 742; DB 4; Length 227;
Best Local Similarity 64.0%; Pred. No. 5.4e-63;
Matches 137; Conservative 24; Mismatches 49; Indels 4; Gaps 3;
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QY 6 QSAHATFYGGGDSAGTGTGCGNLYSTGY-TNTAALSTVLFNDGAACRSCYELRCD-N 63
Db 6 QSAHATFYGGGDSAGTGTGCGNLYSTGY-TNTAALSTVLFNDGAACRSCYELRCD-N 63
QY 64 DGQWCLPG--SVYATATNLCPPNVALPNDGWCNPPRPFMDAEPALQIGYRAGIYP 121
Db 66 QTKWCKRPGGNSLITITATNLCXPMWALPNSGWCNPLKHFDMQSPAMENIAVYQAGIYP 125
QY 122 VSYRRVPCVKKGGIRFTINGSHSYFNLYLVTVNAGPDVQSVISKSSITGMQPSRMNGON 181
Db 126 VNKRYVPXKRGSGIRFPAISGHDYFELVTVTVNAGSGVAVQMSIKGSNTGMAMSRMNGAN 185
QY 182 WQSNAYLDGQSLSEFOYVAVSDGRFTVTSNNVYPAGM 215
Db 186 WQSNAYLAGQSLSFIVQDDGRKVTAMNAPAXM 219
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RESULT 14
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US-08-845-539-6
; Sequence 6, Application US/08845539
; Patent No. 5829303
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,539
FILING DATE: 25-Apr-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-845-539-6
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```
Query Match 57.8%; Score 726.5; DB 2; Length 179;
Best Local Similarity 72.3%; Pred. No. 1.2e-61;
Matches 128; Conservative 18; Mismatches 28; Indels 3; Gaps 2;
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```
QY 10 ATFYGGGDSAGTGTGCGNLYSTGY-TNTAALSTVLFNDGAACRSCYELRCDGQMC 68
Db 3 ATFYGGGDSAGTGTGCGNLYSTGY-TNTAALSTVLFNDGAACRSCYELRCDGQMC 62
QY 69 LRGS--VYVATATNLCPPNVALPNDGWCNPPRPFMDAEPALQIGYRAGIYVSYR 126
Db 63 HPGSPCIFITATNFCPPNVALPNDGWCNPLRTHFDLAMPFLKIAETRAGIGVSYR 122
QY 127 VPCVKKGGIRFTINGSHSYFNLYLVTVNAGPDVQSVISKSSITGMQPSRMNGQMW 183
Db 123 VPCVKKGGIRFTINGSHSYFNLYLVTVNAGPDVQSVISKSSITGMQPSRMNGQMW 179
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RESULT 15
US-09-362-642-6
; Sequence 6, Application US/09362642
; Patent No. 6350935
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
; TITLE OF INVENTION: to Control Fruit Texture and Softening
; FILE REFERENCE: 023070-078210US
; CURRENT APPLICATION NUMBER: US/09/362,642
; CURRENT FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
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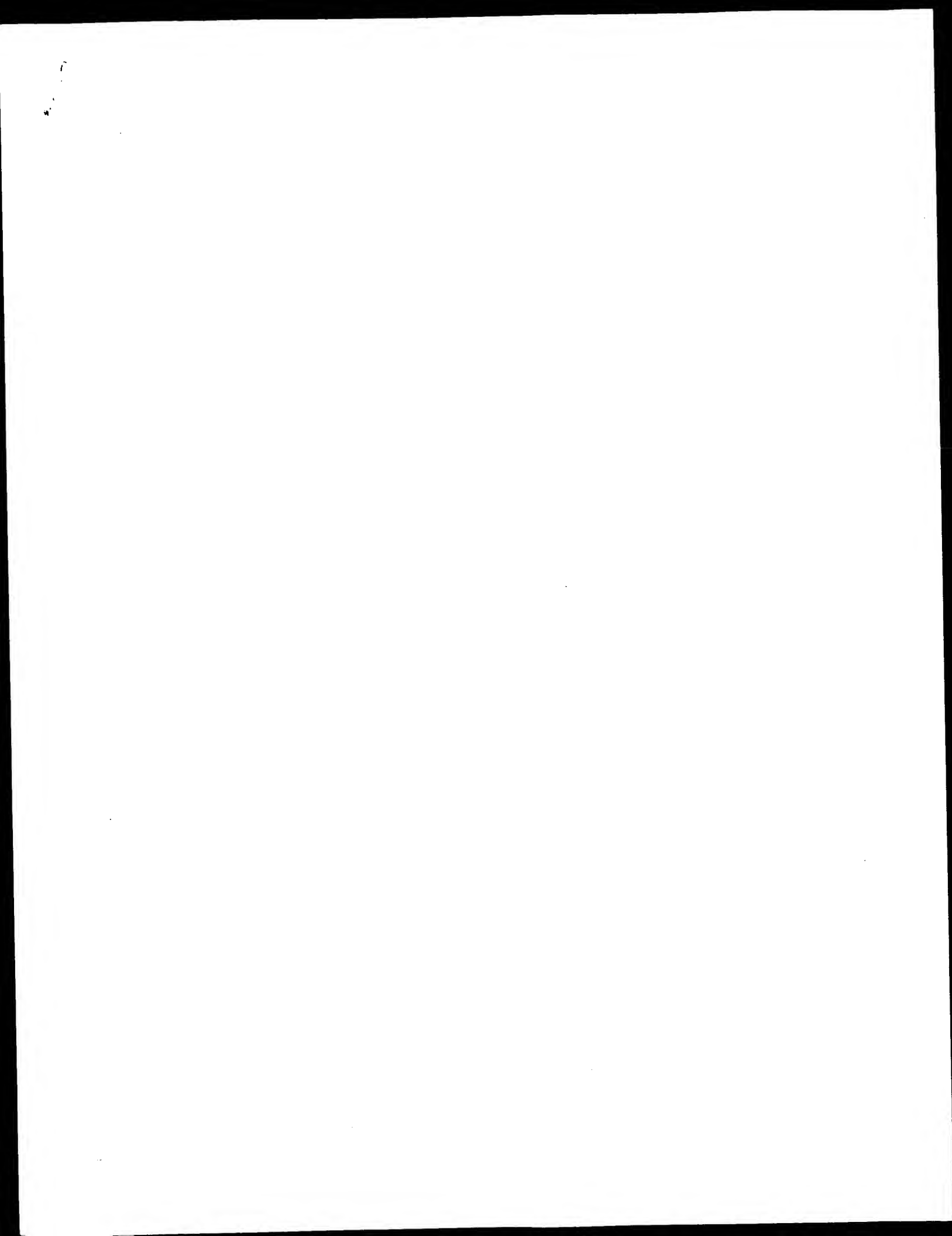
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Cucumis melo
US-09-362-642-6

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Query Match	57.88;	Score 726.5;	DB 4;	Length 179;
Best Local Similarity	72.38;	Pred. No. 1.2e-61;		
Matches 128;	Conservative	18	Matched	36

QY	10	ATATGGGDDASGTMGGCGCGNLTSTGY--TTTATLSTLVFNDCAGACSCYTELRCDNDGQMC	68
Db	3	ATATGGSDDASGTMGCACGCGNLTSTGYGVTATLSTAFVFNNGISGACCEITKCAIDNPRMC	62
QY	69	LPGS--VTTATNLCPNVATLPNDGDMCPPRPHDMMEPAFLDGYRAGIYIPVSYRR	126
Db	63	HPGSPCIFITATNFCPPNFALPNDNGKMLPRTHTDLAMPFLKIAEIRAGIIPVSYRR	122
QY	127	VPCVKKGGCIRPTTINCHSYFNLTAVTNVAGPDVQSYSTIGSSGTGKQPSRRMGNQ	183
Db	123	VPCRKGGCIRPTTINCFRYFNLTAVTNVAGADIVRVSYVAGSNVTGMMSRRMGNQ	179

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Job time : 8.83985 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:49:55 : Search time 25.0184 Seconds
(without alignments)
1003.367 Million cell updates/sec

Title: US-09-896-301-6
Perfect score: 1557
Sequence: 1 DYSWDSAHATFYGGDASC.....NNVVPAGMGEGTPEGGR 226

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246.5	99.2	17	AAR94532	Arabidopsis expans
2	1011.5	80.5	227	AAR94527	Cucumber expansin
3	960.5	76.4	241	AAG06546	Arabidopsis thalia
4	960.5	76.4	241	AAG51633	Arabidopsis thalia
5	960.5	76.4	241	AAG51647	Arabidopsis thalia
6	960.5	76.4	249	AAG06545	Arabidopsis thalia
7	960.5	76.4	249	AAG51632	Arabidopsis thalia
8	960.5	76.4	249	AAG51646	Arabidopsis thalia
9	960.5	76.4	259	AAG06544	Arabidopsis thalia
10	960.5	76.4	259	AAG51631	Arabidopsis thalia
11	960.5	76.4	280	AAG51645	Arabidopsis thalia

12	959.5	76.3	228	17	AAR94528	Rice expansin. Or
13	948	75.4	253	21	AAG25443	Arabidopsis thalia
14	948	75.4	253	21	AAG46483	Arabidopsis thalia
15	938.5	74.7	251	21	AAG23852	Arabidopsis thalia
16	938.5	74.7	251	21	AAG43343	Arabidopsis thalia
17	938.5	74.7	253	21	AAG23851	Arabidopsis thalia
18	938.5	74.7	253	21	AAG43342	Arabidopsis thalia
19	938.5	74.7	253	22	AAG43341	Arabidopsis thalia
20	938.5	74.7	281	21	AAG43341	Arabidopsis thalia
21	938.5	74.7	282	21	AAG23850	Arabidopsis thalia
22	932.5	74.2	250	22	AAG00414	Tomato seed expans
23	903.5	71.9	262	21	AAG29931	Arabidopsis thalia
24	903.5	71.9	273	21	AAG29930	Arabidopsis thalia
25	900	71.6	241	21	AAG05453	Arabidopsis thalia
26	900	71.6	249	21	AAG05452	Arabidopsis thalia
27	900	71.6	255	21	AAG05451	Arabidopsis thalia
28	899.5	71.6	257	21	AAG36445	Arabidopsis thalia
29	895	71.2	242	21	AAG36570	Arabidopsis thalia
30	895	71.2	249	21	AAG36569	Arabidopsis thalia
31	895	71.2	255	21	AAG36568	Arabidopsis thalia
32	880.5	70.0	250	21	AAG09622	Arabidopsis thalia
33	880.5	70.0	258	21	AAG09621	Arabidopsis thalia
34	880.5	70.0	280	21	AAG09620	Arabidopsis thalia
35	871	69.3	257	22	AAG00413	Tomato seed expans
36	864.5	68.8	255	21	AAG30325	Arabidopsis thalia
37	864.5	68.8	257	21	AAG30324	Arabidopsis thalia
38	864	68.7	207	21	AAG25444	Arabidopsis thalia
39	864	68.7	207	21	AAG46484	Arabidopsis thalia
40	863.5	68.7	225	17	AAR94531	Arabidopsis thalia
41	816	64.9	221	21	AAG15694	Arabidopsis thalia
42	816	64.9	221	21	AAG51013	Arabidopsis thalia
43	816	64.9	255	21	AAG15693	Arabidopsis thalia
44	816	64.9	255	21	AAG51012	Arabidopsis thalia
45	815.5	64.9	210	21	AAG29932	Arabidopsis thalia

ALIGNMENTS

RESULT 1
ID AAR94532 standard; Protein; 227 AA.
XX AAR94532:
XX
AC AAR94532:
XX
XX 08-JUL-1996 (first entry)
XX
DE Arabidopsis expansin.
XX
KW Expansin: plant cell wall; cellulose; paper recycling; de-linking;
KM polysaccharide.
XX
XX Arabidopsis sp.
OS
XX
XX AAR94532
XX
XX 04-APR-1996.
XX
XX 12-MAY-1994; 94AU-0068320.
XX
XX 12-MAY-1995; 95US-0440517.
XX
XX 12-MAY-1993; 93US-0060944.
XX
XX (PENN-) PENN STATE RES FOUND.
XX
XX Cosgrove DJ, McQueen-Mason S;
XX WPL; 1996-201150/21.
XX
XX Expansin proteins which alter the mechanical strength of
XX poly(saccharide(s)) - useful in paper mfr. and recycling
XX
XX Disclosure; Page 32-33; 60pp; English.

XX Expansins are a novel class of proteins that catalyze the extension
 CC of plant cell walls and the weakening of the hydrogen bonds in pure
 CC cellulose. 2 Expansins (AAR94528 and AAR94529) have been identified in
 CC rice and 3 in Arabidopsis (AAR94530-32). A cDNA clone (AAT13320)
 CC coding for cucumber expansin 29 (AAR94527) has been obtained. Expansins
 CC can be used e.g. in the mfr., de-linking and recycling of paper, in
 CC the textile industry, to aid delignification processes, to alter gel
 CC mechanical strength, etc.

XX Sequence 227 AA:

Query Match 99.2%; Score 1246.5; DB 17; Length 227;
 Best Local Similarity 99.6%; Pred. No. 4.4e-113;
 Matches 226; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DYSSWQSAHATFPYGGDASGTMGTCGYGNLYSTGYTNTAALSTVLFNDGAACRSCYELR 60
 DB 1 DYSSWQSAHATFPYGGDASGTMGTCGYGNLYSTGYTNTAALSTVLFNDGAACRSCYELR 60
 QY 61 CDNDGQWCLPGSVYTVATNLCPENYALPNDGQWCPNPPRHFDMAPAFLOIGYRAGIV 120
 DB 61 CDNDGQWCLPGSVYTVATNLCPENYALPNDGQWCPNPPRHFDMAPAFLOIGYRAGIV 120
 QY 121 PVSYRRVPCYKKGIRFTINGHSYENLVLTNVAAGPDVQSVSIKSSRTGQPMRSRNMG 180
 DB 121 PVSYRRVPCYKKGIRFTINGHSYENLVLTNVAAGPDVQSVSIKSSRTGQPMRSRNMG 180
 QY 181 NMQSNSTYLDGQSLSFQYAVSDGRTVTSNNVVPAGMFGQTFFGQGF 226
 DB 181 NMQSNSTYLDGQSLSFQYAVSDGRTVTSNNVVPAGMFGQTFFGQGF 227

RESULT 2
 AAR94527
 ID AAR94527 standard; Protein; 227 AA.

XX AAR94527;

XX 08-JUL-1996 (first entry)

XX Cucurbit expansin-29.

XX Expansin-29; plant cell wall; cellulose; paper recycling; de-linking;
 KM polysaccharide; cucumber.

XX Cucumis sativus var. Burpee Pickler.

XX A09540262-A.

XX 04-APR-1996.

XX 12-MAY-1994; 94AU-0068320.

XX 12-MAY-1995; 95US-0440517.

XX 12-MAY-1993; 93US-0060944.

XX (PENN-) PENN STATE RES FOUND.

XX Cosgrove DJ, McQueen-Mason S;

XX WPI; 1996-201150/21.

XX N-PSDB; AAT13320.

XX Expansin proteins which alter the mechanical strength of
 PT polysaccharide(s) - useful in paper mfr. and recycling

XX Claim 7; Page 30; 60pp; English.

XX Cucurbit expansin-29 (AAR94527) is a member of a novel class of
 CC proteins that catalyze the extension of plant cell walls and the
 CC weakening of the hydrogen bonds in pure cellulose. It can be obtained
 CC by expression of an isolated cDNA clone (see AAT13320) in bacterial or

CC other host cells. Expansin proteins have also been identified in oat
 CC coleoptiles, in Arabidopsis (see AAR94530-32) and in rice (AAR94528-29).
 CC and appear to be broadly distributed throughout the plant kingdom.
 CC Expansins can be used e.g. in the mfr., de-linking and recycling of
 CC paper, in the textile industry, to aid delignification processes, to
 CC alter gel mechanical strength, etc.

XX Sequence 227 AA:

Query Match 80.5%; Score 1011.5; DB 17; Length 227;
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QY 1 DYSSWQSAHATFPYGGDASGTMGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 59
 DB 1 DYSSWQSAHATFPYGGDASGTMGACGCGNLYSGYGTNTAALSTVLFNDGACGACFEM 60
 QY 60 RCDNDGQWCLPGSVYTVATNLCPENYALPNDGQWCPNPPRHFDMAPAFLOIGYRAGI 119
 DB 61 TCTNDPCKWCLPGTIRVATNFCPPNFALPNNNGWCPNPPLOHFMABAPAFLOIAOYRAGI 120
 QY 120 VPVSYRRVPCYKKGIRFTINGHSYENLVLTNVAAGPDVQSVSIKSSRTGQPMRSRNMG 179
 DB 121 VPVSYRRVPCYKKGIRFTINGHSYENLVLTNVAAGPDVQSVSIKSSRTGQPMRSRNMG 180
 QY 180 QNMQSNSTYLDGQSLSFQYAVSDGRTVTSNNVVPAGMFGQTFFGQGF 226
 DB 181 QNMQSNSTYLDGQSLSFQYAVSDGRTVTSNNVVPAGMFGQTFFGQGF 227

RESULT 3
 AAG06546
 ID AAG06546 standard; Protein; 241 AA.

XX AAG06546;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 3357.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

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Query Match 76.4%; Score 960.5; DB 21; Length 241;
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DB 78 DQWKLPGSVTYTATNLCPPNVALPNDGCMCNPPRPHDMAEPALDGYRACIVPVS 133
QY 124 YRRVPCRRRGCTIRFTINGSHSYFNVLVTNAGPCDVOSYSIKSSSTGNOPMNRNKGQNMW 183
DB 138 YRRVPCRRRGCTIRFTINGSHSYFNVLVTNAGPCDVOSYSIKSSSTGNOPMNRNKGQNMW 197
QY 184 SNSYLDGQSLFQVAVSDGRTVTSNNVVPAGMOFGCTFEGGCF 226
DB 198 SNSYLDGQSLFQVAVSDGRTVTSNNVVPAGMOFGCTFEGGCF 240

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RESULT 5
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AC AAGS1647;
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 DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 65570.

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

PN EF1033405-A2.

XX EF1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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PR 22-SEP-1999; 99US-0155139.

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PR 29-OCT-1999; 99US-0162142.

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Query Match 76.4%; Score 960.5; DB 21; Length 249;
 Best Local Similarity 75.3%; Pred. No. 3; 2e-85;
 Matches 168; Conservative 22; Mismatches 32; Indels 1; Gaps 1;

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RESULT 9
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AC AAG06544;
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 DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 3355.
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KW Protein identification; signal transduction pathway; metabolic pathway;
 hybridisation assay; genetic mapping; gene expression control; promoter;
 termination sequence.

XX Arabidopsis thaliana.
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XX
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XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Query Match 76.4%; Score 960.5; DB 21; length 259;
Best Local Similarity 75.3%; Pred. No. 3.3e-85;
Matches 168; Conservative 22; Mismatches 32; Indels 1; Gaps 1;

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QY 64 DGQWCLPGSVTVATNLCIPNYALPNDGCMCPRPHPMAEPALQIOTIVYRAGIVPVS 123
DB 96 DGKWCCLPGSVTVATNLCIPNNALANNNGCMCPLEHEDLAPVORIKQIRAGIVPVS 155
QY 124 YRRVPCVKKCGIRPTINGHSYFNLVLTNVAGGQVQSVISKSSGTGQPMRNNQNM 183
DB 156 YRRVPCRRRCGIRFTINGHSYFNLVLTNVGAGDVHSAIKSRTVWQMSRNNQNM 215
QY 184 SNSYLDGOSLFOVAVSDGRTVSNVNPAGMOPGQTEFGGQF 226
DB 216 SNSYLDGOSLFOVAVSDGRTVSNVNPAGMOPGQTEFGGQF 258

RESULT 10
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AC AAG51631;
XX 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 65549.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
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Query Match 76.4%; Score 960.5; DB 21; Length 259;
Best Local Similarity 75.3%; Fred. No. 3.3e-85;
Matches 168; Conservative 22; Mismatches 32; Indels 1; Gaps 1;

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DB 96 DGRWCLPGSVTYTATNFCPPNNAANNNGWCNPLEHFDLAQPVFORIAQYRAGIVEVS 155
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
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XX PF 25-FEB-2000; 2000EP-0301439.
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KM hybridisation assay: genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
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PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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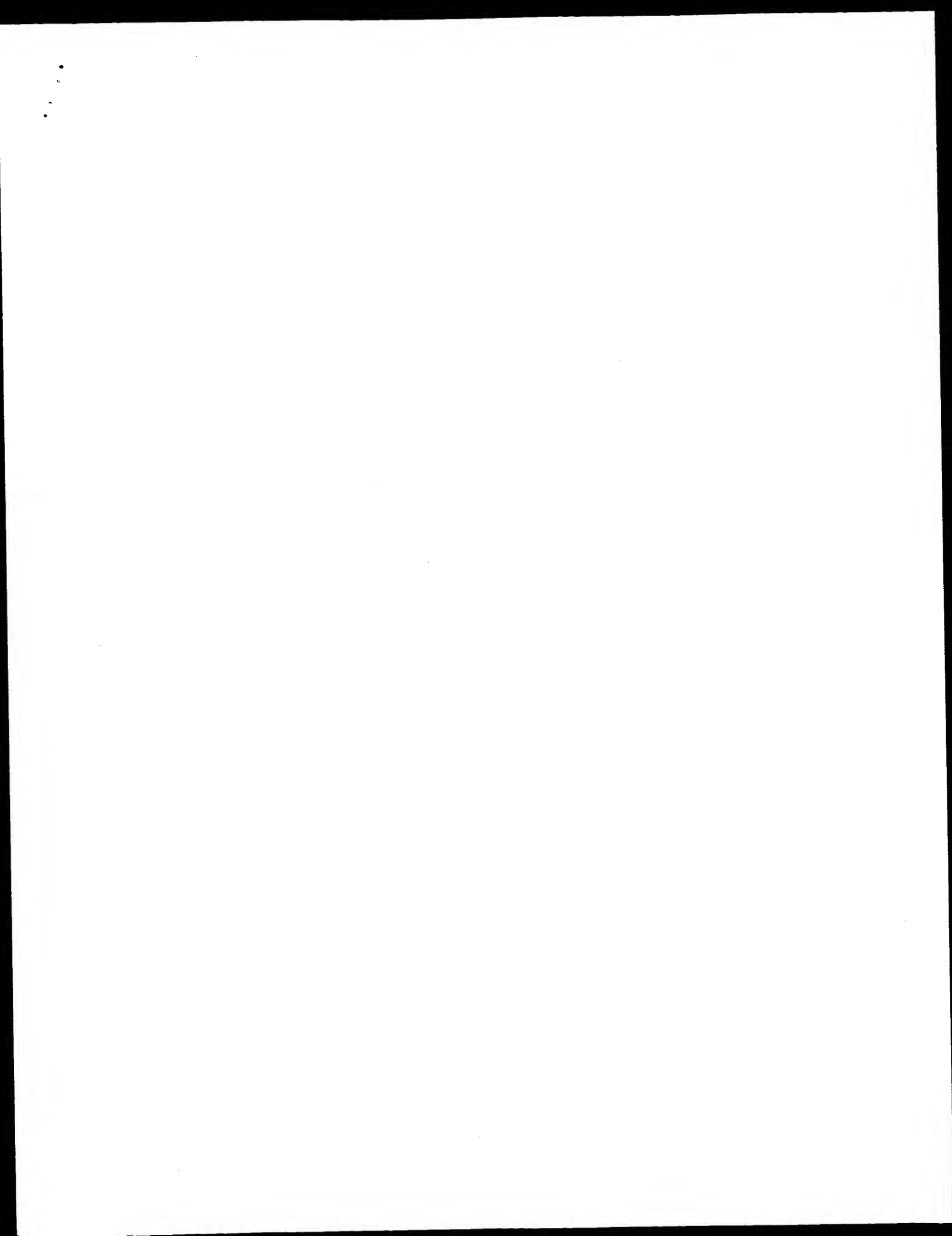
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
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PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159293.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-0144334.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159329.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144684.	PR	14-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0144814.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161982.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0162142.
PR	05-AUG-1999;	99US-0147302.			
PR	05-AUG-1999;	99US-0147312.			
PR	05-AUG-1999;	99US-0147260.			
PR	06-AUG-1999;	99US-0147303.			
PR	06-AUG-1999;	99US-0147416.			
PR	09-AUG-1999;	99US-0147493.			
PR	09-AUG-1999;	99US-0147935.			
PR	10-AUG-1999;	99US-0148171.			
PR	11-AUG-1999;	99US-0148319.			
PR	12-AUG-1999;	99US-0148341.			
PR	13-AUG-1999;	99US-0148565.			
PR	13-AUG-1999;	99US-0148564.			
</					

[illegible][illegible]



GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: October 11, 2002, 14:51:00 ; Search time 19.6007 seconds
(without alignments)
2003.488 Million cell updates/sec

Title: US-09-896-301-7

Perfect score: 1275
Sequence: 1 DYGWQSHAFYGGGASG.....AYNLVPSNMWEGQYEGPOF 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1265	99.2	250	10	Q39625 cucumis sat
2	1143	89.6	254	10	Q82093 prunus ame
3	1138	89.3	245	10	Q91LB2 zinnia eleg
4	1134	88.9	254	10	Q9FNU3 prunus aviu
5	1134	88.9	260	10	Q9FNU0 cicer ariet
6	1105.5	88.7	253	10	Q9SBT1 fragaria an
7	1103.5	86.5	252	10	Q93XP2 prunus cera
8	1101	86.4	252	10	Q9FS30 prunus pers
9	1095	85.9	232	10	Q81133 prunus ame
10	1092	85.6	253	10	Q93493 prunus taeda
11	1092	85.6	253	10	Q9SWT1 prunus taeda
12	1087	85.3	232	10	Q93492 pinus taeda
13	1085	85.1	232	10	P93495 pinus taeda
14	1084	85.0	247	10	Q82625 lycopersico
15	1081.5	84.8	253	10	Q9SWD4 rumex palus
16	1077	84.5	232	10	P93494 pinus taeda

17	1072.5	84.1	253	10	Q22874 arabidopsis
18	1071	84.0	249	10	Q92P35 nicoitina t
19	1056	82.8	251	10	Q94671 oryza sativ
20	1042	81.7	246	10	Q94630 oryza sativ
21	1042	81.7	249	10	Q93XP1 prunus cera
22	1041	81.6	246	10	P93442 oryza sativ
23	1041	81.6	251	10	Q40636 oryza sativ
24	1041	81.6	258	10	Q49194 gossypium h
25	1037	81.3	253	10	Q94KT7 zea mays (m
26	1032	80.9	252	10	Q9FNU2 prunus avu
27	1031	80.9	249	10	Q9LDR9 arabidopsis
28	1027	80.5	237	10	Q38863 arabidopsis
29	1027	80.5	250	10	Q9C554 arabidopsis
30	1026	80.5	247	10	Q9M517 trichysaria
31	1022.5	80.2	255	10	Q38866 arabidopsis
32	1019	79.9	248	10	Q80622 arabidopsis
33	1017	79.8	249	10	Q92P36 nicoitiana t
34	1016.5	79.7	255	10	Q9FLC5 arabidopsis
35	1014.5	79.6	249	10	Q9M515 trichysaria
36	997.5	78.2	242	10	Q9LBB1 zinnia eleg
37	997	78.2	250	10	Q9FVQ9 lycopersico
38	993	77.9	220	10	Q9AYR1 eustoma gra
39	985	77.3	257	10	Q48818 arabidopsis
40	967	75.8	239	10	Q92P31 lycopersico
41	960	75.3	255	10	Q9FMA0 arabidopsis
42	960	75.3	260	10	Q9M2S9 arabidopsis
43	958	75.1	257	10	Q9SD24 marsilea qu
44	954	74.8	262	10	Q80932 arabidopsis
45	953.5	74.8	252	10	Q9FY30 festuca pra

ALIGNMENTS

RESULT 1

Q39625 PRELIMINARY; PRT; 250 AA.
ID Q39625;
AC Q39625;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EXPANSIN S1.
GN CS-EXPI.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Cucurbitales; Cucurbitaceae; Cucumns.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BURPEE PICKLER;
RX MEDLINE=96016146; PubMed=7568110;
RA Shoberhan T.Y., Shi J., Duracko D.M., Gultinan M.J.,
McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansins--a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
DR EMBL; U30382; AA837746.1; -
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSIN.FAMILY.
DR ProDom; PD002179; Pollen_allergen; 1.
FT CHAIN 24
SQ SEQUENCE 250 AA; 27215 MW; 60651BC47E4186DA CRC64;

Query Match 99.2%; Score 1265; DB 10; Length 250;
Best Local Similarity 99.1%; Pred. No. 1.5e-108;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGWQSHAFYGGGASGTCGACGCGNLXSGYGTNTVALSTALFNNGLSCGACFEM 60
DB 24 DYGWQSHAFYGGGASGTCGACGCGNLXSGYGTNTVALSTALFNNGLSCGACFEM 83

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QY 61 TCTNDPKWCLPGTTRVATNFCPPNFALPNDGCKNCPPLQHFDMAPFLQIAQYRAGI 120
    |||
DB 84 TCTNDPKWCLPGTTRVATNFCPPNFALPNDGCKNCPPLQHFDMAPFLQIAQYRAGI 143
QY 121 VPSFRRVPCMKKGVRFTINGHSYFNVLVLTIVGAGADVHSVSIKSRFGWQMSRNNG 180
    |||
DB 144 VPSFRRVPCMKKGVRFTINGHSYFNVLVLTIVGAGADVHSVSIKSRFGWQMSRNNG 203
QY 181 QNWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 227
    |||
DB 204 QNWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 250

RESULT 2
082093
ID 082093 PRELIMINARY; PRT; 254 AA.
AC 082093;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EXPANSIN.
GN PA-EXPI.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Rosaceae; Amygdaloidae; Prunus.
OC NCBI_TaxID=365596;
RN [1]
RP SEQUENCE FROM N.A.
RC SRRATIN-BERGERON; TISSUE=MESOCARP PLUS EXOCARP;
RA Miegite-A-Miegite D., Gomez R.-M., Fils-Lycaon B.;
RT "Molecular cloning and nucleotide sequence of expansin 1 (Pa-Exp1)
    from apricot fruit."
RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL: U93167; AAC3529.1; -.
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen. 1.
DR PRINTS: PR01225; EXPANSINFAMLY.
DR PRODOM: PD002179; Pollen_allergen; 1.
DR PRODOM: PD002179; Pollen_allergen; 1.
SQ SEQUENCE 254 AA; 27264 MW; 88068BD75932FDD0E1 CRC64;

Query Match 89.6%; Score 1143; DB 10; Length 254;
Best Local Similarity 87.2%; Pred. No. 2.5e-97;
Matches 196; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 DYGGWQGHATFYGGDASGTMGAGCYGNLYSGYGTNTVALSTALFNNGSCGACFEF 60
    |||
DB 28 DYGGWQGHATFYGGDASGTMGAGCYGNLYSGYGTNTVALSTALFNNGSCGACFEF 87
QY 61 TCTNDPKWCLPGTTRVATNFCPPNFALPNDGCKNCPPLQHFDMAPFLQIAQYRAGI 120
    |||
DB 88 RCNNDPRKRCRPGSLITVATNFCPPNFALPNDGCKNCPPLQHFDMAPFLQIAQYRAGI 147
QY 121 VPSFRRVPCMKKGVRFTINGHSYFNVLVLTIVGAGADVHSVSIKSRFGWQMSRNNG 180
    |||
DB 148 VPSFRRVPCMKKGVRFTINGHSYFNVLVLTIVGAGADVHSVSIKSRFGWQMSRNNG 207
QY 181 QNWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 227
    |||
DB 208 QNWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 254

RESULT 3
091LB2 PRELIMINARY; PRT; 245 AA.
ID 091LB2;
AC 091LB2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EXPANSIN 2.
OS Zinnia elegans.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Zinnia.
OC NCBI_TaxID=34245;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20317189; PubMed=10859177;
RA Im K.H., Cosgrove D.J., Jones A.M.;
RT "Subcellular localization of expansin mRNA in xylem cells."
RL Plant Physiol. 123:463-470(2000).
DR EMBL: AF230332; AAF35901.1; -.
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSINFAMLY.
DR PRODOM: PD002179; Pollen_allergen; 1.
DR PRODOM: PD002179; Pollen_allergen; 1.
SQ SEQUENCE 245 AA; 26201 MW; F66E26114C27E360 CRC64;

Query Match 89.3%; Score 1138; DB 10; Length 245;
Best Local Similarity 86.7%; Pred. No. 7e-97;
Matches 196; Conservative 19; Mismatches 11; Indels 0; Gaps 0;

QY 2 YGGWQGHATFYGGDASGTMGAGCYGNLYSGYGTNTVALSTALFNNGSCGACFEF 61
    |||
DB 20 YGGWQGHATFYGGDASGTMGAGCYGNLYSGYGTNTVALSTALFNNGSCGACFEF 79
QY 62 TCTNDPKWCLPGTTRVATNFCPPNFALPNDGCKNCPPLQHFDMAPFLQIAQYRAGI 121
    |||
DB 80 CNDPDKWCLPGSLITVATNFCPPNFALPNDGCKNCPPLQHFDMAPFLQIAQYRAGI 139
QY 122 VPSFRRVPCMKKGVRFTINGHSYFNVLVLTIVGAGADVHSVSIKSRFGWQMSRNNG 181
    |||
DB 140 PISFGVPCVKKGVRFTINGHSYFNVLVLTIVGAGADVHSVSIKSRFGWQMSRNNG 199
QY 182 QNWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 227
    |||
DB 200 QNWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 245

RESULT 4
09FUM3 PRELIMINARY; PRT; 254 AA.
ID 09FUM3;
AC 09FUM3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EXPANSIN 1.
GN EXP1 OR EXP2.
OS Prunus avium (Cherry), and
OS Prunus cerasus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Rosaceae; Amygdaloidae; Prunus.
OC NCBI_TaxID=42229, 140311;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P. avium;
RA Wu Z., Wiersma P.A.;
RT "Differential Expression of Expansin Genes Isolated from Sweet Cherry
    (Prunus avium L.) During Fruit Ripening."
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=P. cerasus; TISSUE=RIPENING FRUIT;
RA Yoo S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.;
RT "Coordinated expression of genes encoding expansins and other cell
    wall-modifying enzymes is associated with pectin-related changes in
    the cell wall during ripening of cherry (P. cerasus) fruit."
RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF297521; AAG13982.1; -.
DR EMBL: AF350937; AAK4846.1; -.
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSINFAMLY.

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Best Local Similarity 82.7%; Pred. No. 1,1e-92;
Matches 186; Conservative 22; Mismatches 17; Indels 0; Gaps 0;

OY 2 YGWMOSGHAATFYGGDASGTMGACGYGNTLSQGYGTNTVALSTALFNNGLSGACACEMT 61
DB 7 YGWMESAHATFYGGSDASGTMGACGYGNTLSQGYGTNTVALSTALFNNGLSGACACEMR 66
OY 62 CTNDPKMCLPCTIRYATATNFCPPNFALPNDGCMCNPLDHPDMAEPALQIAQYRAGIV 121
DB 67 CNDPQWMLPCTVYATATNFCPPNFALPNDGCMCNPLDHPDMAEPALQIAQYRAGIV 126
OY 122 PVSFRVPCMKKGVRTTNGHSYFNVLITNVGAGADVHSYISKSRGQMSRMNQ 181
DB 127 PLYTRVPCLRKGGIRFTVNGHSYFNVLITNVGAGADVHAIVISKSRSGQMPMSRMNQ 186
OY 182 NMOSNNYLNQGLSFQVTLSDGRTLTAAYLVPSNMOPGQTEGPO 226
DB 187 NMOSNNYLNQGLSFQVTLSDGRTLTAAYLVPSNMOPGQTEGPO 231

RESULT 11

O9SMY1

ID O9SMY1

PRELIMINARY;

PRT: 253 AA.

AC O9SMY1: 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE EXPANSIN.
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOCOTYL;
RX MEDLINE=99329318; PubMed=10398718;
RA Hutchison K.W., Singer P.B., McIntosh S., Diaz-Sala C., Greenwood M.S.;
RT "Expansins are conserved in conifers and expressed in hypocotyls in
RT response to exogenous auxin."
RL Plant Physiol. 120:827-832(1999).
DR EMBL: AF085330; AAD47901.1;
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSINFAMILY.
DR Prodom: PD002179; Pollen_allergen; 1.
SQ SEQUENCE 253 AA: 27150 MW: 2675BBI569BD75D4 CRC64;

Query Match 85.6%; Score 1092; DB 10; Length 253;
Best Local Similarity 82.7%; Pred. No. 1,2e-92;
Matches 186; Conservative 22; Mismatches 17; Indels 0; Gaps 0;

OY 2 YGWMOSGHAATFYGGDASGTMGACGYGNTLSQGYGTNTVALSTALFNNGLSGACACEMT 61
DB 28 YGWMESAHATFYGGSDASGTMGACGYGNTLSQGYGTNTVALSTALFNNGLSGACACEMR 87
OY 62 CTNDPKMCLPCTIRYATATNFCPPNFALPNDGCMCNPLDHPDMAEPALQIAQYRAGIV 121
DB 88 CNDPQWMLPCTVYATATNFCPPNFALPNDGCMCNPLDHPDMAEPALQIAQYRAGIV 147
OY 122 PVSFRVPCMKKGVRTTNGHSYFNVLITNVGAGADVHSYISKSRGQMSRMNQ 181
DB 148 PLYTRVPCLRKGGIRFTVNGHSYFNVLITNVGAGADVHAIVISKSRSGQMPMSRMNQ 207
OY 182 NMOSNNYLNQGLSFQVTLSDGRTLTAAYLVPSNMOPGQTEGPO 226
DB 208 NMOSNNYLNQGLSFQVTLSDGRTLTAAYLVPSNMOPGQTEGPO 252

RESULT 12

P93492

ID P93492

PRELIMINARY;

PRT: 232 AA.

AC P93492: 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Created)

DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE EXPANSIN (FRAGMENT).
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOCOTYL;
RX Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
RT "Expansins are conserved in conifers and expressed in response to
RT exogenous auxin."
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64890; AAB40634.1;
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSINFAMILY.
DR Prodom: PD002179; Pollen_allergen; 1.
FT NON_TER 1
SQ SEQUENCE 232 AA: 24734 MW: 1340AF483DE0741F CRC64;

Query Match 85.3%; Score 1087; DB 10; Length 232;
Best Local Similarity 82.2%; Pred. No. 3,2e-92;
Matches 185; Conservative 22; Mismatches 18; Indels 0; Gaps 0;

OY 2 YGWMOSGHAATFYGGDASGTMGACGYGNTLSQGYGTNTVALSTALFNNGLSGACACEMT 61
DB 7 YGWMESAHATFYGGSDASGTMGACGYGNTLSQGYGTNTVALSTALFNNGLSGACACEMR 66
OY 62 CTNDPKMCLPCTIRYATATNFCPPNFALPNDGCMCNPLDHPDMAEPALQIAQYRAGIV 121
DB 67 CNDPQWMLPCTVYATATNFCPPNFALPNDGCMCNPLDHPDMAEPALQIAQYRAGIV 126
OY 122 PVSFRVPCMKKGVRTTNGHSYFNVLITNVGAGADVHSYISKSRGQMSRMNQ 181
DB 127 PLYTRVPCLRKGGIRFTVNGHSYFNVLITNVGAGADVHAIVISKSRSGQMPMSRMNQ 186
OY 182 NMOSNNYLNQGLSFQVTLSDGRTLTAAYLVPSNMOPGQTEGPO 226
DB 187 NMOSNNYLNQGLSFQVTLSDGRTLTAAYLVPSNMOPGQTEGPO 231

RESULT 13

P93495

ID P93495

PRELIMINARY;

PRT: 232 AA.

AC P93495: 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE EXPANSIN (FRAGMENT).
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOCOTYL;
RX Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
RT "Expansins are conserved in conifers and expressed in response to
RT exogenous auxin."
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64893; AAB40637.1;
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSINFAMILY.
DR Prodom: PD002179; Pollen_allergen; 1.
FT NON_TER 1
SQ SEQUENCE 232 AA: 24694 MW: 9238EACD9E1F6C5E CRC64;

Query Match 85.1%; Score 1085; DB 10; Length 232;
Best Local Similarity 82.2%; Pred. No. 4,9e-92;
Matches 185; Conservative 23; Mismatches 17; Indels 0; Gaps 0;

QY 2 YGWSGHATFYGGGASGTMGACGAGNLYSOGYGTNTVALSTALFNNGLSGACFE 61
 DB 7 YGWSGHATFYGGGASGTMGACGAGNLYSOGYGTNTVALSTALFNNGLSGACFE 66
 QY 62 CTNDPKWCLPCTIVATNFCPPNFALPNDGKCNPLDHPMAEPALQIAQYAGIV 121
 DB 67 CNDPOMCLPCTIVATNFCPPNFALPNDGKCNPLDHPMAEPALQIAQYAGIV 126
 QY 122 PVSEFRVPCMKKGVFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGWSMSRNM 181
 DB 127 PLTVRVCPLKGGIRFTVNGHSYFNVLITNVGAGDVHSVSIKSGRTGWSMSRNM 186
 QY 182 NMOSNNYLNQGLSFVYTLSDGRTLTAYNLVPSNMWFGQTEGPO 226
 DB 187 NMOSNNYLNQGLSFVYTLSDGRTLTAYNLVPSNMWFGQTEGPO 231

RESULT 14
 082625 PRELIMINARY; PRT; 247 AA.
 AC 082625;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE EXPANSIN.
 GN LEXP2.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 NCBI_TaxID=4081;
 RX [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=HYPOCOTYL;
 RA Catala C., Rose J.K.C., Bennett A.B.;
 RT "Hormonal regulation and expression patterns of LEXP2, a new tomato
 RT expansin.";
 RT Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV. VEN8;
 RA Caderas D., Muster M., Vogler H., Mandel T., Rose J.,
 RA McQueen-Mason S., Kuhlmeier C.;
 RT "limited correlation between expansin gene expression and elongation
 RT growth rate.";
 RT Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
 RL EMBL; AF096776; AAC64201.1;
 DR EMBL; AJ239068; CAB43197.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 SO SEQUENCE 247 AA; 26470 MW; 995653F84F7A3E1 CRC64;

Query Match 85.0%; Score 1084; DB 10; Length 247;
 Best local Similarity 81.9%; Pred. No. 6, 6e-92;
 Matches 186; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

QY 1 DYGGWSGHATFYGGGASGTMGACGAGNLYSOGYGTNTVALSTALFNNGLSGACFE 60
 DB 21 DYGGWSGHATFYGGGASGTMGACGAGNLYSOGYGTNTVALSTALFNNGLSGACFE 80
 QY 61 TCTNDPKWCLPCTIVATNFCPPNFALPNDGKCNPLDHPMAEPALQIAQYAGI 120
 DB 81 TCTNDPKWCLPCTIVATNFCPPNFALPNDGKCNPLDHPMAEPALQIAQYAGI 140
 QY 121 PVSEFRVPCMKKGVFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGWSMSRNM 180
 DB 141 PVSEFRVPCMKKGVFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGWSMSRNM 200
 QY 181 NMOSNNYLNQGLSFVYTLSDGRTLTAYNLVPSNMWFGQTEGPO 227

DB 201 QNMOSNNYLNQGLSFVYTLSDGRTLTAYNLVPSNMWFGQTEGPO 247

RESULT 15
 09SMD4 PRELIMINARY; PRT; 253 AA.
 ID 09SMD4;
 AC 09SMD4;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE EXPANSIN.
 GN Rumeex palustris.
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllales; Polygonaceae; Rumeex.
 NCBI_TaxID=50298;
 RX [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RA MEDLINE=20330988; PubMed=10872228;
 RA Vriezen W.H., De Graaf B., Mariani C., Voesecke L.A.C.J.;
 RT "Submergence induces expansin gene expression in flooding-tolerant
 RT Rumex palustris and not in flooding-intolerant R. acetosa.";
 RL Planta 210:956-963(2000).
 DR EMBL; AF167360; AAD49956.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 SO SEQUENCE 253 AA; 27063 MW; 7DC75610C80B23A8 CRC64;

Query Match 84.8%; Score 1081.5; DB 10; Length 253;
 Best local Similarity 82.9%; Pred. No. 1, 1e-91;
 Matches 189; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

QY 1 DYGGWSGHATFYGGGASGTMGACGAGNLYSOGYGTNTVALSTALFNNGLSGACFE 59
 DB 26 DYGGWSGHATFYGGGASGTMGACGAGNLYSOGYGTNTVALSTALFNNGLSGACFE 85
 QY 60 TCTNDPKWCLPCTIVATNFCPPNFALPNDGKCNPLDHPMAEPALQIAQYAGI 119
 DB 86 TCTNDPKWCLPCTIVATNFCPPNFALPNDGKCNPLDHPMAEPALQIAQYAGI 145
 QY 120 PVSEFRVPCMKKGVFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGWSMSRNM 179
 DB 146 PVSEFRVPCMKKGVFTINGHSYFNVLITNVGAGDVHSVSIKSGRTGWSMSRNM 205
 QY 180 QNMOSNNYLNQGLSFVYTLSDGRTLTAYNLVPSNMWFGQTEGPO 227
 DB 206 QNMOSNNYLNQGLSFVYTLSDGRTLTAYNLVPSNMWFGQTEGPO 253

Search completed: October 11, 2002, 14:59:43
 Job time : 20.6007 secs

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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:50:30 ; Search time 5.86347 Seconds
(without alignments)
1499.000 Million cell updates/sec

Title: US-09-896-301-7

Perfect score: 1275

Sequence: 1 DYGMQSGHATFYGGDASG.....AYNLVPSNMQFGQTECPGR 227

Scoring table: BLOSUM62

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	231.5	18.2	263	1	MPPI_PHLPR
2	229.5	18.0	265	1	MPPI_HOLLA
3	227.5	17.8	263	1	MPPI_LOLPR
4	225	17.6	246	1	MPPI_CINDA
5	216.5	17.0	269	1	MPPI_PHAQA
6	192.5	15.1	263	1	MPPI_ORYSA
7	185	14.5	191	1	MPPI_MAIZE
8	106.5	8.4	242	1	GUNS_TRIRE
9	100.5	7.9	316	1	Y007_CHLTR
10	97.5	7.6	181	1	GUN_MYRED
11	96	7.5	333	1	CATJ_MOUSE
12	95.5	7.5	2871	1	FBN1_MOUSE
13	93.5	7.3	2871	1	FBN1_BOVIN
14	92	7.2	1385	1	YMS5_CAEEL
15	89.5	7.0	1429	1	L112_CAEEL
16	89	7.0	677	1	SP87_DICDI
17	88.5	6.9	894	1	ILP3_HUMAN
18	87.5	6.9	316	1	Y275_CHLMU
19	87.5	6.9	2871	1	FBN1_HUMAN
20	87.5	6.9	2871	1	FBN1_PIG
21	85	6.7	154	1	KRSC_CHICK
22	84	6.6	386	1	KR87_DROME
23	83.5	6.5	633	1	C2AD_BACTU
24	83	6.5	82	1	KRHA_SHEEP
25	82	6.4	207	1	EGG2_SCHUA
26	82	6.4	212	1	EGG1_SCHUA
27	82	6.4	645	1	K22E_HUMAN
28	79.5	6.2	684	1	FBL1_CHICK
29	79	6.2	493	1	CHT1_RHINI
30	79	6.2	2005	1	CIN2_HUMAN
31	79	6.2	5265	1	FBOH_BOVMO
32	78.5	6.2	283	1	POR3_BOVIN
33	78.5	6.2	283	1	POR3_RABIT

34	78	6.1	571	1	FLA1_CAME	P56963 campylobact
35	77.5	6.1	574	1	FLA3_CAME	Q46113 campylobact
36	77	6.0	465	1	GRP2_PHAVU	P10496 phaeocystis v
37	77	6.0	1325	1	YDEK_ECOLI	P32051 escherichia
38	76.5	6.0	283	1	POR3_HUMAN	Q92777 homo sapien
39	76.5	6.0	283	1	POR3_MOUSE	O60931 mus musculu
40	76.5	6.0	489	1	ABF8_ASPNG	P42255 aspergillus
41	76.5	6.0	680	1	PBP2_STRPN	P10524 streptococc
42	76.5	6.0	1456	1	MANR_HUMAN	P22897 homo sapien
43	76	6.0	373	1	ADHX_RABIT	O19053 oryctolagus
44	76	6.0	385	1	PER_DROME	P1666 drosophila
45	76	6.0	593	1	KIC1_HUMAN	P13645 homo sapien

ALIGNMENTS

RESULT 1	ID	MPPI_PHLPR	STANDARD:	PRT:	263 AA.
AC	P43213:				
DT	01-NOV-1995 (Rel. 32, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DE	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Pollen allergen Phl p 1 precursor (Phl p I).				
GN	PHLP.				
OS	Phleum pratense (Common timothy).				
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:				
OC	Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Poideae:				
OC	Poaceae: Phleum.				
ON	NCBI_Taxid=15957;				
OX	(1)				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Pollen;				
RX	MEDLINE=95015525; PubMed=7930302;				
RA	Laffer S., Valente R., Vrtala S., Susani M., van Ree R., Kraft D.,				
RA	Schneider O., Duchene M.;				
RT	*Complementary DNA cloning of the major allergen Phl p 1 from timothy				
RT	grass (Phleum pratense); recombinant Phl p I inhibits IgE binding to				
RT	group I allergens from eight different grass species *;				
RL	J. Allergy Clin. Immunol. 94:689-698(1994).				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- SIMILARITY: BELONGS TO THE LOI p I FAMILY OF ALLEGENS.				
CC	-1- SIMILARITY: CONTAINS 1 EXPANSTIN-LIKE EG45 DOMAIN.				
CC	-1- SIMILARITY: CONTAINS 1 EXPANSTIN-LIKE CBD DOMAIN.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL: X78813; CAA55390.1; -				
DR	HSSP: P43214; WHO.				
DR	InterPro: IPR000882; Pollen.allergen.				
DR	Pfam: PF01357; Pollen.allergen.1.				
DR	PRINTS: PR01225; EXPANSTIN.FAMILY.				
DR	ProDom: P0002179; Pollen.allergen.1.				
DR	PROSITE: PS50843; EXPANSTIN.CBD; 1.				
DR	PROSITE: PS50842; EXPANSTIN.EG45; 1.				
KW	Allergen: Glycoprotein; Signal: Multigene family.				
FT	SIGNAL	1	23		POTENTIAL.
FT	CHAIN	24	263		POLLEN ALLERGEN PHL P 1.
FT	DOMAIN	61	167		EXPANSTIN-LIKE EG45.
FT	DOMAIN	181	262		EXPANSTIN-LIKE CBD.
FT	CARBOHYD	32	32		N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	263 AA;	28457 MM;		Q46BA249C17BC048 CRC64;

Query Match 18.2% Score 231.5; DB 1; Length 263;
Best Local Similarity 27.6% Pred. No. 6.2e-13;
Matches 67; Conservative 41; Mismatches 96; Indels 39; Gaps 11;

Y 2 YGC-WQSGHATFYGGGASGTM--GGACGYGNLYSOGYGTNTVALSTALFNNGISGCAF 58
 Db 37 YGDKMLDAKSTWYKPTGAKRNDGACGYKDVDPKPPSGMTGCGNTPIFKSGGCSGF 96
 Y 59 EMTCTNDPKWCL--PGTIRVATNFCPPNFALPNDGWCNPL--QHFDMAEPALQIA 114
 Db 97 EIKCTK-PEACSGEPVYVHTIDN-----EPIAPYHFDLSGHAFGMA 139
 Y 115 Q-----YRAGIVPSFRPVCCKKGGVRFITN----GHSYFNLVLTITNGAGADVHSV 163
 Db 140 KKGEOKRLRSAGELELQRRVCKKTPGCTKTFHYEKGSNPNYLLALVYKYNAGDDVAV 199
 Y 164 SIK-GSRTGQMSMRNMGONQ--SNNYLNGGSLFOVTLSDGRTLTAYNLVPSNMQFGQ 220
 Db 200 DIKKGKDKWIELKESMGAVVRVDPKLTGP-FTVRYTTEGGKTEAEADVIEGKMDT 258
 Y 221 TYE 223
 Db 259 SYE 261

RESULT 2
 MPIL_HOLLA STANDARD: PRT: 265 AA.
 ID MPIL_HOLLA
 AC P43216; Q39975;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Major pollen allergen Hol 1 precursor (Hol 1 I) (Hol 1 I.0101 and 1.0102).
 OS Holcus lanatus (Velvet grass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Poaceae; Holcus.
 NC NCBL_TaxID=29679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. AVENEA; TISSUE-Pollen;
 RA Schramm G.D., Bufe A., Becker W.M., Schlaak M.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBD databases.
 RN [2]
 RP SEQUENCE OF 18-265 FROM N.A.
 RC STRAIN-CV. AVENEA; TISSUE-Pollen;
 RA MEDLINE-97358126; PubMed-9215246;
 RT Schramm G.D., Bufe A., Petersen A., Haas H., Schlaak M., Becker W.M.;
 RT "Mapping of IgE-binding epitopes on the recombinant major group I allergen of velvet grass pollen, Hol 1 I.";
 RT J. Allergy Clin. Immunol. 99:781-787(1997).
 RN [3]
 RP CHARACTERIZATION.
 RC STRAIN-CV. AVENEA; TISSUE-Pollen;
 RA MEDLINE-96319506; PubMed-8768803;
 RT Schramm G.D., Petersen A., Bufe A., Schlaak M., Becker W.M.;
 RT "Identification and characterization of the major allergens of velvet grass (Holcus lanatus), Hol 1 I and Hol 1 5.";
 RT Int. Arch. Allergy Immunol. 110:354-363(1996).
 RL 1. SUBCELLULAR LOCATION: Secreted.
 CC 1. SIMILARITY: BELONGS TO THE LIL P I FAMILY OF ALLERGENS.
 CC 1. SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
 CC 1. SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
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 CC
 DR EMBL; Z27084; CA81610.1; -;
 DR EMBL; Z68893; CA93121.1; -;
 DR HSSP; P43214; IWHO.

DR InterPro: IPR000882; Pollen.allergen.
 DR Pfam: PF01357; Pollen.allergen.1.
 DR PRINTS: PR01225; EXPANSINFAMLT.
 DR ProDom: PD002179; Pollen.allergen.1.
 DR PROSITE: PS50843; EXPANSIN_CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 KW Allergen; signal.
 FT SIGNAL. 1 25 POTENTIAL.
 FT CHAIN 26 265 MAJOR POLLEN ALLERGEN HOL 1 I.
 FT DOMAIN 63 169 EXPANSIN-LIKE EG45.
 FT DOMAIN 183 264 EXPANSIN-LIKE CBD.
 FT VARIANT 103 103 T -> S (IN HOL 1 I.0102).
 SQ SEQUENCE 265 AA; 28590 MW; 1FE23B3BE198AD6D CRC64;
 Query Match 18.0%; Score 229.5; DB 1; Length 265;
 Best Local Similarity 27.6%; Pred. No. 9.3e-13;
 Matches 67; Conservative 41; Mismatches 96; Indels 39; Gaps 11;
 Y 2 YGC-WQSGHATFYGGGASGTM--GGACGYGNLYSOGYGTNTVALSTALFNNGISGCAF 58
 Db 39 YGDEMILDAKSTWYKPTGAKRNDGACGYKDVDPKPPSGMTGCGNTPIFKSGGCSGF 98
 Y 59 EMTCTNDPKWCL--PGTIRVATNFCPPNFALPNDGWCNPL--QHFDMAEPALQIA 114
 Db 99 EIKCTK-PEACSGEPVYVHTIDN-----EPIAPYHFDLSGHAFGMA 141
 Y 115 Q-----YRAGIVPSFRPVCCKKGGVRFITN----GHSYFNLVLTITNGAGADVHSV 163
 Db 142 KKGEOKRLRSAGELELQRRVCKKTPGCTKTFHYEKGSNPNYLLALVYKYNAGDDVAV 201
 Y 164 SIK-GSRTGQMSMRNMGONQ--SNNYLNGGSLFOVTLSDGRTLTAYNLVPSNMQFGQ 220
 Db 202 DIKKGKDKWIELKESMGAVVRVDPKLTGP-FTVRYTTEGGKTEAEADVIEGKMDT 260
 Y 221 TYE 223
 Db 261 AYE 263

RESULT 3
 MPIL_LOLPR STANDARD: PRT: 263 AA.
 ID MPIL_LOLPR
 AC P14946; P19964;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Pollen allergen Lol p I precursor (Lol p I) (Allergen R7).
 OS Lolium perenne (Perennial ryegrass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Poaceae; Lolium.
 NC NCBL_TaxID=4522;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-90375479; PubMed-1697854;
 RA Perez M., Ishoka G.Y., Walker L.E., Chesnut R.W.;
 RT "cDNA cloning and immunological characterization of the rye grass allergen Lol p I.";
 RT J. Biol. Chem. 265:16210-16215(1990).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-48.
 RC TISSUE-Pollen;
 RA MEDLINE-91160716; PubMed-2001733;
 RA Griffith I.J., Smith P.M., Pollock J., Theerakulpisut P., Avjoglu A., Davies S., Hough T., Singh M.B., Simpson R.J., Ward L.D., Knox R.B.;
 RT "Cloning and sequencing of Lol pI, the major allergenic protein of rye-grass pollen.";
 RT FEBS Lett. 279:210-215(1991).
 RN [3]
 RP SEQUENCE OF 24-53.
 RC TISSUE-Pollen;
 RA MEDLINE-86242068; PubMed-3718469;

Db 179 IKPRUSDDEFIMKSSWGAIMRIDPKKPLKGFSTRLTSEGCAHLVQDVJLPAANKPPTVY 238

RESULT 5
MPAL_PHAQ STANDARD; PRT: 269 AA.
ID MPAL_PHAQ 041260;
AC 041260;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Major pollen allergen Pha a 1 precursor (Pha a 1).
OS Phalaris aquatica (Canary grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Phalaris.
ON NCBI_TaxID=28479;
RX MEDLINE=96105569; Pubmed=8564724;
RP TISSUE=Pollen;
RC SEQUENCE FROM N.A.
RA Suphioglu C., Singh M.B., Simpson R.J., Ward L., Knox R.B.;
RT "Cloning, sequencing and expression in Escherichia coli of Pha a 1
RT and four isoforms of Pha a 5, the major allergens of canary grass
RT pollen.";
RL Clin. Exp. Allergy 25:853-865(1995).
RN [2]
RP SEQUENCE OF 30-49.
RX MEDLINE=93319091; Pubmed=7687099;
RA Suphioglu C., Singh M.B., Simpson R.J., Ward L., Knox R.B.;
RT "Identification of canary grass (Phalaris aquatica) pollen allergens
RT by immunoblotting: IgE and IgG antibody-binding studies.";
RL Allergy 48:273-281(1993).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
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CC
CC EMBL: S80654; AAB35984.1; -.
DR HSSP: P43214; IMHO.
DR InterPro: IPR000882; Pollen.allergen.
DR Pfam: PF01357; Pollen.allergen. 1.
DR PRINTS: PR01225; EXPANSINFAMILY.
DR PRODOM: PD002179; Pollen.allergen. 1.
DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 269 MAJOR POLLEN ALLERGEN PHA A 1.
FT DOMAIN 67 173 EXPANSIN-LIKE EG45.
FT DOMAIN 187 268 EXPANSIN-LIKE CBD.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 37 37 P -> G (IN REF. 2).
FT SEQUENCE 269 AA; 29011 MW; 05883A458AC877F CRC64;
Query Match 17.0%; Score 216.5; DB 1; Length 269;
Best Local Similarity 26.9%; Pred. No. 1.2e-11;
Matches 64; Conservative 42; Mismatches 93; Indels 39; Gaps 11;

Db 102 FELKCSK-PSCSGEPIVTHITDDN-----EPIIAPHFDLSGHAFGSM 144

QY 114 AQ-----YRAGIVPSFRPRVPCMKKGVFTIN-----GHSFNLVLITNNGAGDIVIS 162
DB 145 AKGGEENVNAGAELELOEFRVCKYPDGTPTFHEKSGNPYYALLKRYVDGDDVVA 204
QY 163 VSRIG-SRRTGQSMRNRWGNMQ--SNNYLNGGLSFQVTLSDGPTLUTFVNLVPSNMQ 217
DB 205 VDIKKGKDKMVKELKESWGAIMRIDPKLTGP-FIVRTTBGTAEFEVDYIPESK 261

RESULT 6
MPOL_ORYSA STANDARD; PRT: 263 AA.
ID MPOL_ORYSA 040638;
AC 040638;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Major pollen allergen Ory s 1 precursor (Ory s 1).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriaralioideae; Oryzaceae; Oryza.
ON NCBI_TaxID=4530;
RX MEDLINE=96069591; Pubmed=7590339;
RA Xu H., Theerakulpisut P., Goulding N., Suphioglu C., Singh M.B.,
RA Bhalla P.L.;
RT "Cloning, expression and immunological characterization of Ory s 1,
RT the major allergen of rice pollen.";
RL Gene 164:255-259(1995).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MATURE ANTHELS BUT NOT IN
CC VEGETATIVE OR OTHER FLORAL TISSUES.
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
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CC
CC EMBL: U31771; AAB6533.1; -.
DR HSSP: P43214; IMHO.
DR InterPro: IPR000882; Pollen.allergen.
DR Pfam: PF01357; Pollen.allergen. 1.
DR PRINTS: PR01225; EXPANSINFAMILY.
DR PRODOM: PD002179; Pollen.allergen. 1.
DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 263 MAJOR POLLEN ALLERGEN ORY S 1.
FT DOMAIN 61 164 EXPANSIN-LIKE EG45.
FT DOMAIN 178 259 EXPANSIN-LIKE CBD.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 263 AA; 28497 MW; B1C5F24EA398DD60 CRC64;
Query Match 15.1%; Score 192.5; DB 1; Length 263;
Best Local Similarity 28.5%; Pred. No. 1.4e-09;
Matches 59; Conservative 36; Mismatches 77; Indels 35; Gaps 11;

OY 80 NECPNFALPNDGWCNPL--QHEDMAEPALQIAQ---YRAGIVPSFRBPCCK 133
 DB 119 N-----DEPIAAYHEDLSGLAMKDGDEELRKAGLITDTRRVRCKYP 162
 OY 134 GGVRFIN---GHSYFNLVLTNNVGAGADVHSYI--KSGRTGQMSRNMQMSNN 187
 DB 163 ADRTKEFHEKASNPNNYLALLVKYVAGDGVVEVEIKKESGEE-WKALKESGALWIRDT 221
 OY 188 YLNGOC-LSFOYTLSDGRTITAYNLVP 213
 DB 222 PKPLKGPSVRYTTEGARSSMEDAIP 248

RESULT 7

MP21_MAIZE STANDARD: PRT: 191 AA.
 AC 007154:
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE Pollen allergen Zea m 1 (Zea m 1).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OK NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pollen;
 RX MEDLINE=94010312; PubMed=8406014;
 RA Broadwater A.H., Rudinstein A.L., Chay C.H., Klapper D.G.,
 RA Bedinger P.A.;
 RT "Zea m1, the maize homolog of the allergen-encoding lol p1 gene of
 RT rye grass.";
 RL Gene 131:227-230(1993).
 CC -1- TISSUE SPECIFICITY: POLLEN TISSUE.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION LOW BEFORE AND HIGH AFTER
 CC POLLEN MITOSIS.
 CC -1- DISEASE: CAUSES MAIZE POLLEN ALLERGY.
 CC -1- SIMILARITY: BELONGS TO THE LOL P 1 FAMILY OF ALLERGENS.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 CC
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DR EMBL: U4271; AAA33496.1; -
 DR PIR: JCI524; JCI524.
 DR HSSP: P43214; IMHO.
 DR MaltEDB: 65840; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen.1.
 DR PRINTS: PR01225; EXPANSIN_FAMLY.
 DR ProDom: PD002179; Pollen_allergen.1.
 DR PROSITE: PS50843; EXPANSIN_CBD.
 DR PROSITE: PS50842; EXPANSIN_EG45.1.
 KW Allergen; Multigene family.
 FT DOMAIN 1 91 EXPANSIN-LIKE EG45.
 FT SIGNAL 105 186 EXPANSIN-LIKE CBD.
 SO SEQUENCE 191 AA; 21362 MW; 6E2A9DF921C45C63 CRC64;

Query Match 14.5%; Score 185; DB 1; Length 191;
 Best Local Similarity 26.3%; Pred. No. 4.2e-09;
 Matches 52; Conservative 36; Mismatches 80; Indels 30; Gaps 8;

OY 40 TVALSTALNNGLSCACFEMCTNDPKWCL--PGTIRVATINCPNFALPNDGWCN 97

DB 2 TACGNVPIFKDGKCGSCYEVCKEKEPE-CSGNPVTEITDMNPE---IAP----- 49
 OY 98 PLOHEDMAEPALQIAQ-----YRAGIVPSFRBPCCKKGGVRRITNGHSYFN--- 147
 DB 50 ---YHEDLSGKAFGLSLAKGLNDKLRHGINDEYRRYKRCYIPGOKLVFIIEKGCNNY 106
 OY 148 -LVLTNNVGAGADVHSYISIKSGRTG-WQMSRNMQMSNNYLNNGOC-LSFOYTLSDGR 204
 DB 107 VAVLVKFEVADDDIVLMEIODKLSAEMKPMKLSMGAIWRMDTAAALAGPFSIRLTSLSGK 166
 OY 205 TLTAVALVPSNMQFGQTY 222
 DB 167 KVIAKDIIPANKRPDAVY 184

RESULT 8

GUN5_TRIPE STANDARD: PRT: 242 AA.
 AC P43317:
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)
 DE (Cellulase V) (EG V).
 OS Trichoderma reesei (Hypocrea jecorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Hypocreaceae; Hypocrea.
 OK NCBI_TaxID=51453;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=QM9414 / RUT C-30;
 RX MEDLINE=95075308; PubMed=7984103;
 RA Saloheimo A., Henriksat B., Hoffren A.-M., Telemann O., Penttilae M.,
 RA "A novel, small endoglucanase gene, eg15, from Trichoderma reesei
 RT isolated by expression in yeast.";
 RL Mol. Microbiol. 13:219-228(1994).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY K (FAMILY 45 OF GLYCOSYL
 CC HYDROLASES).
 CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
 CC
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DR EMBL: Z33381; CAAB3846.1; -
 DR HSSP: P00725; ZCBH.
 DR InterPro: IPR000254; CBD_fungal.
 DR InterPro: IPR000334; Glyco_hydro_45.
 DR Pfam: PF00734; CBD_1; 1.
 DR Pfam: PF02015; Glyco_hydro_45; 1.
 DR ProDom: PD001821; CBD_fungal; 1.
 DR SMART: SM00236; fcbd; 1.
 DR PROSITE: PS00362; CBD_FUNGAL; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 DR PROSITE: PS01140; GLYCOSYL_HYDROL_F45; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Signal.
 FT CHAIN 1 17 POTENTIAL.
 FT ACT_SITE 18 242 ENDOGLUCANASE V.
 FT ACT_SITE 27 27 NUCLEOPHILE (BY SIMILARITY).
 FT DOMAIN 134 134 PROTON DONOR (BY SIMILARITY).
 FT DOMAIN 183 182 CATALYTIC.
 FT DOMAIN 183 205 PRO/SER-RICH (LINKER).
 FT CARBOHYD 206 242 CELLULOSE-BINDING (BY SIMILARITY).
 FT DISULFID 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 213 230 BY SIMILARITY.
 FT DISULFID 224 240 BY SIMILARITY.

AC Q9R014; Q9WV51;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cathepsin J precursor (EC 3.4.22.-) (Cathepsin P) (CatLp-P).
 GN CTSJ OR CTSJP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RA MEDLINE=9456833; PubMed=10526153;
 RT Tisjar K., Deussing J., Peters C.;
 RT "Cathepsin J, a novel murine cysteine protease of the papain family
 RT with a placenta-restricted expression.";
 RL FEBS Lett. 459:299-304(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Placenta;
 RA Sol-Church K., Frenck J., Troeber D., Mason R.W.;
 RT "Cloning of a mouse cysteine protease.";
 RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Lysosomal (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 CC PAPAIN FAMILY OF THIOL PROTEASES.
 CC -----
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 CC -----
 DR EMBL: AF136272; AF133142.1;
 DR EMBL: AF158182; AA041898.1;
 DR HSSP: P07711; ICUL.
 DR MEROPS: C01.038;
 DR MGD: MGI:1349426; Ctsj.
 DR InterPro: IPR000668; Peptidase_C1.
 DR InterPro: IPR000169; Thiolprol_act_site.
 DR Pfam: PF00112; Peptidase_C1; 1.
 DR PRINTS: PR00705; PAPAIN.
 DR PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
 DR PROSITE: PS00640; THIOL_PROTEASE_ASN; 1.
 KW Hydrolyase; Thiol protease; Glycoprotein; Lysosome; Zymogen; Signal.
 FT SIGNAL 1 17
 FT PROPEP 18 112
 FT CHAIN 113 333
 FT ACT_SITE 137 137
 FT ACT_SITE 275 275
 FT ACT_SITE 299 299
 FT ACT_SITE 134 177
 FT DISULFID 168 210
 FT DISULFID 268 321
 FT CARBOHYD 71 71
 FT CARBOHYD 216 216
 FT CARBOHYD 220 220
 FT CARBOHYD 267 267
 FT CONFLICT 42 42
 SQ SEQUENCE 333 AA: 37147 MW: F9A8FTD5A138721 CRC64;
 P -> PK (IN REF. 2).
 Query Match 7.5%; Score 96; DB 1; Length 333;
 Best Local Similarity 23.3%; Pred. No. 0.31;
 Matches 54; Conservative 16; Mismatches 84; Indels 78; Gaps 12;
 QY 1 DYCGM-QSGHAT-----FYGGDASGIMGACG-----YGN 30
 DB 115 DYDMHEGYIVPRNCGCGSCMAFAAGATEGMEFKTGNLPVSQVNLDCSKTVGN 174

QY 31 LYSQGYGTNTVALSTALFNNGISCGACFEMTCTNDPKKLPCTIVYATNF--CPNPAL 88
 DB 175 KCGQS-GTAAQAFELYKKKGLAEATYYPEGKDPCCRYRSENASANTYDVNLPPN--- 230
 QY 89 PNDGGMCEPPIQHFDMAPFLQIAQYRAGIVP-----SFRVPCMKGGVPT 139
 DB 231 -----ELYLMVAV--ASIGPVSAIDASHDSFR---FYMGIIYE 265
 QY 140 INCHSYF--NLVLITVVGAGDYHSYISKGRSGTQMSRMKGQWQMSNNYL 189
 DB 266 PMSSTFVNHAVLVVGYGSEGV-----KDGNNYV-LIKNSMGEPMGNMYM 311
 RESULT 12
 FBNI_BOVIN
 ID FBNI_BOVIN STANDARD: PRT; 2871 AA.
 AC P98133;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibrillin 1 precursor (MP340).
 GN FBNI.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA MEDLINE=95137597; PubMed=7835900;
 RT Tilsta D.J., Potter K.A., Byers P.H.;
 RT "Sequence of the coding region of the bovine fibrillin cDNA and
 RT localization to bovine chromosome 10.";
 RL Genomics 23:480-485(1994).
 RN [2]
 RP PARTIAL SEQUENCE.
 RA MEDLINE=96132851; PubMed=8557636;
 RA Gibson M.A., Hatzinikolas G., Kumarallake J.S., Sandberg L.B.,
 RA Nicholl J.K., Sutherland G.R., Cleary E.G.;
 RT "Further characterization of proteins associated with elastic fiber
 RT microfibrils including the molecular cloning of MAF-2 (MP25).";
 RL J. Biol. Chem. 271:1096-1103(1996).
 CC -1- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
 CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
 CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
 CC -1- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER
 CC FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
 CC MICROFIBRILS.
 CC -1- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING
 CC EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
 CC -----
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 CC -----
 DR EMBL: L28748; AA074122.1;
 DR HSSP: P35555; IAPJ.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001861; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR002212; TB.
 DR Pfam: PF00008; EGF_46.
 DR Pfam: PF00683; TB; 9.
 DR PRINTS: PR00010; EGFLOOD.
 DR SMART: SM00179; EGF_CA; 42.

DR SMART: SM00001: EGF like: 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 43.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 38.
 DR PROSITE; PS01187; EGF_CA; 45.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 KW Repeat: Multigene family.
 FT SIGNAL 1 27
 FT CHAIN 1 2871
 FT DOMAIN 81 112
 FT DOMAIN 115 146
 FT DOMAIN 147 178
 FT DOMAIN 246 287
 FT DOMAIN 288 329
 FT REPEAT 330 390
 FT REPEAT 392 446
 FT DOMAIN 449 489
 FT DOMAIN 490 529
 FT DOMAIN 530 571
 FT DOMAIN 572 612
 FT DOMAIN 613 653
 FT REPEAT 654 722
 FT REPEAT 723 764
 FT DOMAIN 765 806
 FT DOMAIN 807 846
 FT DOMAIN 910 951
 FT REPEAT 952 1027
 FT DOMAIN 1028 1069
 FT DOMAIN 1070 1112
 FT DOMAIN 1113 1154
 FT DOMAIN 1155 1196
 FT DOMAIN 1197 1237
 FT DOMAIN 1238 1279
 FT DOMAIN 1280 1321
 FT DOMAIN 1322 1363
 FT DOMAIN 1363 1403
 FT DOMAIN 1404 1445
 FT DOMAIN 1446 1486
 FT DOMAIN 1487 1527
 FT REPEAT 1528 1605
 FT DOMAIN 1606 1647
 FT REPEAT 1648 1688
 FT DOMAIN 1689 1765
 FT REPEAT 1766 1807
 FT DOMAIN 1808 1848
 FT DOMAIN 1849 1890
 FT DOMAIN 1891 1929
 FT DOMAIN 1930 1972
 FT DOMAIN 1973 2012
 FT DOMAIN 2013 2054
 FT REPEAT 2055 2126
 FT DOMAIN 2127 2205
 FT DOMAIN 2206 2246
 FT DOMAIN 2247 2290
 FT DOMAIN 2291 2332
 FT REPEAT 2333 2401
 FT DOMAIN 2402 2443
 FT DOMAIN 2444 2484
 FT DOMAIN 2485 2523
 FT DOMAIN 2524 2566
 FT DOMAIN 2567 2606
 FT DOMAIN 2607 2647
 FT DOMAIN 2648 2687
 FT DISULFID 85 94
 FT DISULFID 89 100
 FT DISULFID 102 111
 FT DISULFID 119 129
 FT DISULFID 123 134
 FT DISULFID 136 145
 FT DISULFID 150 160
 FT DISULFID 154 166
 FT DISULFID 168 177

FT DISULFID 250 262 BY SIMILARITY.
 FT DISULFID 257 271 BY SIMILARITY.
 FT DISULFID 273 286 BY SIMILARITY.
 FT DISULFID 292 304 BY SIMILARITY.
 FT DISULFID 299 313 BY SIMILARITY.
 FT DISULFID 315 328 BY SIMILARITY.
 FT DISULFID 453 465 BY SIMILARITY.
 FT DISULFID 460 474 BY SIMILARITY.
 FT DISULFID 476 488 BY SIMILARITY.
 FT DISULFID 494 504 BY SIMILARITY.
 FT DISULFID 499 513 BY SIMILARITY.
 FT DISULFID 515 528 BY SIMILARITY.
 FT DISULFID 534 546 BY SIMILARITY.
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 FT DISULFID 582 596 BY SIMILARITY.
 FT DISULFID 598 611 BY SIMILARITY.
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 FT DISULFID 727 739 BY SIMILARITY.
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 FT DISULFID 750 763 BY SIMILARITY.
 FT DISULFID 769 781 BY SIMILARITY.
 FT DISULFID 776 790 BY SIMILARITY.
 FT DISULFID 792 805 BY SIMILARITY.
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 FT DISULFID 832 845 BY SIMILARITY.
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 FT DISULFID 1265 1278 BY SIMILARITY.
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 FT DISULFID 1326 1339 BY SIMILARITY.
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 FT DISULFID 1367 1380 BY SIMILARITY.
 FT DISULFID 1374 1389 BY SIMILARITY.
 FT DISULFID 1391 1402 BY SIMILARITY.
 FT DISULFID 1408 1420 BY SIMILARITY.
 FT DISULFID 1415 1429 BY SIMILARITY.
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 FT DISULFID 1456 1470 BY SIMILARITY.
 FT DISULFID 1472 1485 BY SIMILARITY.
 FT DISULFID 1491 1502 BY SIMILARITY.
 FT DISULFID 1497 1511 BY SIMILARITY.
 FT DISULFID 1513 1526 BY SIMILARITY.
 FT DISULFID 1610 1622 BY SIMILARITY.

Query Match
 Best Local Similarity

7.5%: Score 95.5; DB 1; Length 2871;
 26.6%: Pred. No. 3.2;

FT	SIGNAL	27	POTENTIAL.
FT	CHAIN	26	FIBRILIN 1.
FT	DOMAIN	81	EGF-LIKE 1, NON-CALCIUM BINDING
FT	DOMAIN	115	EGF-LIKE 2, NON-CALCIUM BINDING
FT	DOMAIN	147	EGF-LIKE 3, NON-CALCIUM BINDING
FT	DOMAIN	246	EGF-LIKE 4, CALCIUM-BINDING
FT	DOMAIN	288	EGF-LIKE 5, CALCIUM-BINDING
FT	DOMAIN	330	EGF-LIKE 6, NON-CALCIUM BINDING
FT	DOMAIN	402	EGF-LIKE 7, CALCIUM-BINDING
FT	DOMAIN	449	EGF-LIKE 8, CALCIUM-BINDING
FT	DOMAIN	490	EGF-LIKE 9, CALCIUM-BINDING
FT	DOMAIN	530	EGF-LIKE 10, CALCIUM-BINDING
FT	DOMAIN	572	EGF-LIKE 11, CALCIUM-BINDING
FT	DOMAIN	613	EGF-LIKE 12, CALCIUM-BINDING
FT	DOMAIN	656	EGF-LIKE 13, CALCIUM-BINDING
FT	DOMAIN	721	EGF-LIKE 14, CALCIUM-BINDING
FT	DOMAIN	753	EGF-LIKE 15, CALCIUM-BINDING
FT	DOMAIN	765	EGF-LIKE 16, CALCIUM-BINDING
FT	DOMAIN	807	EGF-LIKE 17, CALCIUM-BINDING
FT	DOMAIN	910	EGF-LIKE 18, CALCIUM-BINDING
FT	DOMAIN	952	EGF-LIKE 19, CALCIUM-BINDING
FT	DOMAIN	1018	EGF-LIKE 20, CALCIUM-BINDING
FT	DOMAIN	1028	EGF-LIKE 21, CALCIUM-BINDING
FT	DOMAIN	1070	EGF-LIKE 22, CALCIUM-BINDING
FT	DOMAIN	1113	EGF-LIKE 23, CALCIUM-BINDING
FT	DOMAIN	1155	EGF-LIKE 24, CALCIUM-BINDING
FT	DOMAIN	1197	EGF-LIKE 25, CALCIUM-BINDING
FT	DOMAIN	1238	EGF-LIKE 26, CALCIUM-BINDING
FT	DOMAIN	1280	EGF-LIKE 27, CALCIUM-BINDING
FT	DOMAIN	1322	EGF-LIKE 28, CALCIUM-BINDING
FT	DOMAIN	1363	EGF-LIKE 29, CALCIUM-BINDING
FT	DOMAIN	1404	EGF-LIKE 30, CALCIUM-BINDING
FT	DOMAIN	1446	EGF-LIKE 31, CALCIUM-BINDING
FT	DOMAIN	1487	EGF-LIKE 32, CALCIUM-BINDING
FT	DOMAIN	1528	EGF-LIKE 33, CALCIUM-BINDING
FT	DOMAIN	1568	EGF-LIKE 34, CALCIUM-BINDING
FT	DOMAIN	1606	EGF-LIKE 35, CALCIUM-BINDING
FT	DOMAIN	1648	EGF-LIKE 36, CALCIUM-BINDING
FT	DOMAIN	1689	EGF-LIKE 37, CALCIUM-BINDING
FT	DOMAIN	1758	EGF-LIKE 38, CALCIUM-BINDING
FT	DOMAIN	1807	EGF-LIKE 39, CALCIUM-BINDING
FT	DOMAIN	1848	EGF-LIKE 40, CALCIUM-BINDING
FT	DOMAIN	1890	EGF-LIKE 41, CALCIUM-BINDING
FT	DOMAIN	1929	EGF-LIKE 42, CALCIUM-BINDING
FT	DOMAIN	1930	EGF-LIKE 43, CALCIUM-BINDING
FT	DOMAIN	1973	EGF-LIKE 44, CALCIUM-BINDING
FT	DOMAIN	2013	EGF-LIKE 45, CALCIUM-BINDING
FT	DOMAIN	2055	EGF-LIKE 46, CALCIUM-BINDING
FT	DOMAIN	2127	EGF-LIKE 47, CALCIUM-BINDING
FT	DOMAIN	2166	EGF-LIKE 48, CALCIUM-BINDING
FT	DOMAIN	2205	EGF-LIKE 49, CALCIUM-BINDING
FT	DOMAIN	2246	EGF-LIKE 50, CALCIUM-BINDING
FT	DOMAIN	2287	EGF-LIKE 51, CALCIUM-BINDING
FT	DOMAIN	2331	EGF-LIKE 52, CALCIUM-BINDING
FT	DOMAIN	2381	EGF-LIKE 53, CALCIUM-BINDING
FT	DOMAIN	2402	EGF-LIKE 54, CALCIUM-BINDING
FT	DOMAIN	2443	EGF-LIKE 55, CALCIUM-BINDING
FT	DOMAIN	2484	EGF-LIKE 56, CALCIUM-BINDING
FT	DOMAIN	2533	EGF-LIKE 57, CALCIUM-BINDING
FT	DOMAIN	2574	EGF-LIKE 58, CALCIUM-BINDING
FT	DOMAIN	2606	EGF-LIKE 59, CALCIUM-BINDING
FT	DOMAIN	2647	EGF-LIKE 60, CALCIUM-BINDING
FT	DOMAIN	2687	EGF-LIKE 61, CALCIUM-BINDING
FT	DOMAIN	271	EGF-LIKE 62, CALCIUM-BINDING
FT	DOMAIN	273	EGF-LIKE 63, CALCIUM-BINDING
FT	DOMAIN	292	EGF-LIKE 64, CALCIUM-BINDING
FT	DOMAIN	299	EGF-LIKE 65, CALCIUM-BINDING
FT	DOMAIN	304	EGF-LIKE 66, CALCIUM-BINDING
FT	DOMAIN	313	EGF-LIKE 67, CALCIUM-BINDING
FT	DOMAIN	328	EGF-LIKE 68, CALCIUM-BINDING
FT	DOMAIN	335	EGF-LIKE 69, CALCIUM-BINDING
FT	DOMAIN	453	EGF-LIKE 70, CALCIUM-BINDING

FT	DISULFID	460	474	BY SIMILARITY.
FT	DISULFID	476	488	BY SIMILARITY.
FT	DISULFID	494	504	BY SIMILARITY.
FT	DISULFID	499	513	BY SIMILARITY.
FT	DISULFID	515	528	BY SIMILARITY.
FT	DISULFID	534	546	BY SIMILARITY.
FT	DISULFID	541	555	BY SIMILARITY.
FT	DISULFID	557	570	BY SIMILARITY.
FT	DISULFID	576	587	BY SIMILARITY.
FT	DISULFID	582	596	BY SIMILARITY.
FT	DISULFID	598	611	BY SIMILARITY.
FT	DISULFID	617	628	BY SIMILARITY.
FT	DISULFID	623	637	BY SIMILARITY.
FT	DISULFID	639	652	BY SIMILARITY.
FT	DISULFID	727	739	BY SIMILARITY.
FT	DISULFID	734	748	BY SIMILARITY.
FT	DISULFID	750	763	BY SIMILARITY.
FT	DISULFID	769	781	BY SIMILARITY.
FT	DISULFID	776	790	BY SIMILARITY.
FT	DISULFID	792	805	BY SIMILARITY.
FT	DISULFID	811	821	BY SIMILARITY.
FT	DISULFID	816	830	BY SIMILARITY.
FT	DISULFID	832	845	BY SIMILARITY.
FT	DISULFID	914	926	BY SIMILARITY.
FT	DISULFID	921	935	BY SIMILARITY.
FT	DISULFID	937	950	BY SIMILARITY.
FT	DISULFID	1032	1044	BY SIMILARITY.
FT	DISULFID	1039	1053	BY SIMILARITY.
FT	DISULFID	1055	1068	BY SIMILARITY.
FT	DISULFID	1074	1086	BY SIMILARITY.
FT	DISULFID	1081	1095	BY SIMILARITY.
FT	DISULFID	1097	1111	BY SIMILARITY.
FT	DISULFID	1117	1129	BY SIMILARITY.
FT	DISULFID	1124	1138	BY SIMILARITY.
FT	DISULFID	1140	1153	BY SIMILARITY.
FT	DISULFID	1159	1171	BY SIMILARITY.
FT	DISULFID	1166	1180	BY SIMILARITY.
FT	DISULFID	1182	1195	BY SIMILARITY.
FT	DISULFID	1201	1212	BY SIMILARITY.
FT	DISULFID	1208	1221	BY SIMILARITY.
FT	DISULFID	1223	1236	BY SIMILARITY.
FT	DISULFID	1242	1254	BY SIMILARITY.
FT	DISULFID	1249	1263	BY SIMILARITY.
FT	DISULFID	1265	1278	BY SIMILARITY.
FT	DISULFID	1284	1296	BY SIMILARITY.
FT	DISULFID	1291	1305	BY SIMILARITY.
FT	DISULFID	1307	1320	BY SIMILARITY.
FT	DISULFID	1326	1339	BY SIMILARITY.
FT	DISULFID	1333	1348	BY SIMILARITY.
FT	DISULFID	1350	1361	BY SIMILARITY.
FT	DISULFID	1367	1380	BY SIMILARITY.
FT	DISULFID	1374	1389	BY SIMILARITY.
FT	DISULFID	1391	1402	BY SIMILARITY.
FT	DISULFID	1408	1420	BY SIMILARITY.
FT	DISULFID	1415	1429	BY SIMILARITY.
FT	DISULFID	1431	1444	BY SIMILARITY.
FT	DISULFID	1450	1461	BY SIMILARITY.
FT	DISULFID	1456	1470	BY SIMILARITY.
FT	DISULFID	1472	1485	BY SIMILARITY.
FT	DISULFID	1491	1502	BY SIMILARITY.
FT	DISULFID	1497	1511	BY SIMILARITY.
FT	DISULFID	1513	1526	BY SIMILARITY.
FT	DISULFID	1610	1622	BY SIMILARITY.
FT	DISULFID	1617	1631	BY SIMILARITY.
FT	DISULFID	1633	1646	BY SIMILARITY.
FT	DISULFID	1652	1663	BY SIMILARITY.
FT	DISULFID	1658	1672	BY SIMILARITY.

[illegible]

RESULT 14	YMS5_CAEEL	STANDARD:	PRT: 1385 AA.
YMS5_CAEEL	YMS5_CAEEL		
ID	YMS5_CAEEL	STANDARD:	PRT: 1385 AA.
AC	P34501;		
DT	01-FEB-1994 (Rel. 28, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Hypothetical 159.2 kDa protein K03H1.5 in chromosome III.		
GN	K03H1.5.		
OS	<i>Caenorhabditis elegans</i> .		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		

[illegible]

DR EMBL; Z29560; CAA82664.1; -.
DR PIR; S41028; S41028.
DR WormPeP; KO3H1.5; CE03459.
DR InterPro; IPR002909; IPT_TIG.
DR InterPro; IPR003886; Nidogen_ext.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR InterPro; IPR001846; Vwd.
DR Pfam; PF00094; vwd; 1.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00429; IPT; 1.
DR SMART; SM00539; NIDO; 1.
DR SMART; SM00216; VWD; 1.
DR Hypothetical protein.
SQ SEQUENCE 1385 AA; 159181 MW; BDCD8F59CEA38C03 CRC64;

Query Match 7.2%; Score 92; DB 1; Length 1385;
Best Local Similarity 23.0%; Pred. No. 3;
Matches 50; Conservative 26; Mismatches 73; Indels 68; Gaps 10.

```

QY      2 YGWSGSHATFYGGDASGTMG-GACGCGNYSOGYGTNIVALTALFNNGLSGCAQEFM 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     399 FGGKAAMAGF-NGNGNGTGYCLPYSGGRLMKLGY-----FSVNLPGRWIHR 446
QY      61 T-----CTNDPKMKLPGTIRVATNFCPPNALPNDGGMCPQLQ---HFDMAEP 108

```



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FT DISULFID 408 419 BY SIMILARITY.
FT DISULFID 413 429 BY SIMILARITY.
FT DISULFID 431 440 BY SIMILARITY.
FT DISULFID 507 518 BY SIMILARITY.
FT DISULFID 512 529 BY SIMILARITY.
FT DISULFID 531 540 BY SIMILARITY.
FT DISULFID 547 558 BY SIMILARITY.
FT DISULFID 552 567 BY SIMILARITY.
FT DISULFID 569 578 BY SIMILARITY.
FT DISULFID 586 597 BY SIMILARITY.
FT DISULFID 591 607 BY SIMILARITY.
FT DISULFID 609 618 BY SIMILARITY.
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 751 751 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 754 754 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 900 900 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1429 AA: 157115 MW: 2555EDD7A62C025DB CRC64:

```

```

Query Match 7.0%: Score 89.5; DB 1; Length 1429;
Best Local Similarity 30.0%; Pred. No. 5.1;
Matches 27; Conservative 6; Mismatches 36; Indels 21; Gaps 4;

```

```

QY 13 YGGGDSAGTMG--GACGYGNLYSGYGTNYALSTALFNNGISGACAFEMTCTNDPKWCL 70
DB 663 FDGGDSCSKREPFPSKCRGNCACAD-----FPANGVCNQACNNECLYDGMDCCL 710

```

```

QY 71 PGTIR--VTATNCPNPFALPNDGWCNP 98
DB 711 PAVVRCPVKIREHCASRFA-----NGICDP 735

```

Search completed: October 11, 2002, 14:57:37
 Job time : 7.86347 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:53:05 : Search time 11.3919 seconds
(without alignments)
1914.721 Million cell updates/sec

Title: US-09-896-301-7

Perfect score: 1275
Sequence: 1 DYGMQSGHATFYGGGDSAG.....AYNLVPSNMWQFGQTEGPOF 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1265	99.2	250	2	T10079
2	1092	85.6	232	2	T09821
3	1087	85.3	232	2	T09818
4	1085	85.1	232	2	T09825
5	1077	84.5	232	2	T09825
6	1072.5	84.1	253	2	T04831
7	1041	81.6	246	2	T04175
8	1041	81.6	251	2	T03298
9	1041	81.6	258	2	T09786
10	1027	80.5	237	2	T50654
11	1022.5	80.2	245	2	T50656
12	1019	79.9	248	2	C84444
13	985	77.3	257	2	D84820
14	960	75.3	260	2	T47689
15	954	74.8	262	2	T02530
16	947	74.3	261	2	T07630
17	945	74.1	257	2	T50658
18	940	73.7	255	2	T06573
19	939	73.6	257	2	T02727
20	939	73.6	259	2	T50653
21	937	73.5	258	2	S53082
22	935	73.3	264	2	T50659
23	934	73.3	260	2	T48247
24	934	73.3	258	2	T08016
25	924	72.5	262	2	T50660
26	889.5	69.8	255	2	T50655
27	874	68.5	258	2	T10083
28	859.5	67.4	261	2	T03737
29	853.5	67.1	252	2	F86335

30	832	65.3	255	2	T02010
31	819.5	64.3	255	2	T03299
32	730	57.3	160	2	T09871
33	678	53.2	257	2	G36654
34	668	52.4	257	2	F86259
35	604	47.4	256	2	T05648
36	322.5	25.3	102	2	T09828
37	317	24.9	77	2	T09815
38	280	22.0	81	2	T09830
39	278	21.8	259	2	T50657
40	278	21.8	271	2	H84592
41	276	21.6	277	2	S48032
42	271	21.3	261	2	T04301
43	270.5	21.2	491	2	F96681
44	266.5	20.9	259	2	F84886
45	242	19.0	262	2	S38620

ALIGNMENTS

RESULT 1

T10079
expansin S1 precursor - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T10079

R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gullitman, M.J.; McQueen-Mason, S.J.; Shi
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995

A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
A:Reference number: 214894; MUID:96016146
A:Accession: T10079

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-250 <SHC>

A:Cross-references: EMBL:U30382; NID:g1040874; PIDN:AB37746.1; PID:g1040875
A:Experimental source: cultivar Burpee Pickler
C:Genetics:

A:Gene: EXP1
C:Function:
A:Description: mediates cell wall extension
C:Superfamily: expansin

F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-250/Product: expansin #status predicted <MAT>

Query Match 99.2% Score 1265; DB 2; Length 250;
Best Local Similarity 99.1% Pred. No. 3.9e-102;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1	DYGMQSGHATFYGGGDSAGTGMGACGYGNYSGCYGTNTVALSTALPNNNGSGACFEM	60
DB	24	DYGMQSGHATFYGGGDSAGTGMGACGYGNYSGCYGTNTVALSTALPNNNGSGACFEM	83
QY	61	TCTNDPKMCLPCTIRYATNFCPPNFALPNDGNCNPLQHFDAEPAFLQIAVRAGI	120
DB	84	TCTNDPKMCLPCTIRYATNFCPPNFALPNNNGCNPPLQHFDAEPAFLQIAVRAGI	143
QY	121	VVVSRRRVCKMKGGVRFPTINSHFNVLVTINVGAGADYHSVTSKGSRTGQMSRWMC	180
DB	144	VVVSRRRVCKMKGGVRFPTINSHFNVLVTINVGAGADYHSVTSKGSRTGQMSRWMC	204
QY	181	QNMOSNNYLNQGLSFQVTLSDGRITLTAYNLVPNMWQFGQTEGPOF	227
DB	204	QNMOSNNYLNQGLSFQVTLSDGRITLTAYNLVPNMWQFGQTEGPOF	250

RESULT 2

T09821
expansin (clone pTexp3) - jobiolly pine (fragment)

C:Species: Pinus taeda (loblolly pine)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09821

R:Hutchinson, K.W.; Slinger, P.B.; Diaz-Sala, C.; Greenwood, M.S.

submitted to the EMBL Data Library, July 1996

A:Description: Expansins are conserved in conifers and expressed in response to exogenous

A:Reference number: Z16866

A:Accession: T09821

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-232 <HUT>

A:Cross-references: EMBL:U64891; NID:g1778100; PID:g1778101

A:Experimental source: clone pteexp3

C:Superfamily: expansin

Query Match

Best Local Similarity 85.6%; Score 1092; DB 2; Length 232;

Matches 186; Conservative 22; Mismatches 17; Indels 0; Gaps 0;

Db

2 YGWMOSGATFTYGGDSAGTGMGACGYGNLYSGYGTNTVALSTALFNNGLSGACFEWT 61

7 YGWMESAHATFTYGGDSAGTGMGACGYGNLYSGYGTNTVALSTALFNNGLSGACFEWT 66

62 CTNDPKMCLPGTIRYATATNCPNFPALPNDGWCNPPLOHFDMAEPALQIAQYRAGIV 121

67 CNDPQWCLPGTYVTATNCPNFPALPNDGWCNPPLOHFDMAEPALQIAQYRAGIV 126

122 PVSEFRVPCMKKGGVFTINGHSYFNLYLTNVGAGDVHSVSIKSRGTGQMSRMWGQ 181

127 PLYTRVPCLRKGGIRFTVNGHSYFNLYLTNVGAGDVHVAHSIKSRSGWQPSRMWGQ 186

182 NMOSNNYLTNGGSLSFQVTLSDGRTLTAYNLVPSNMFGQTYEGPQ 226

187 NMOSNYLTNGGSLSFQVTLSDGRTVSNNAVPNMFGQTYEGSQ 231

RESULT 3

T09818

expansin (clone pteexp2) - loblolly pine (fragment)

C:Species: Pinus taeda (loblolly pine)

C>Date: 16-Jul-1999 #sequence-revision 16-Jul-1999 #text-change 26-May-2000

C:Accession: T09818

R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.

submitted to the EMBL Data Library, July 1996

A:Description: Expansins are conserved in conifers and expressed in response to exogenous

A:Reference number: Z16866

A:Accession: T09818

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-232 <HUT>

A:Cross-references: EMBL:U64890; NID:g1778098; PID:g1778099

A:Experimental source: clone pteexp2; hypocotyl

C:Superfamily: expansin

Query Match

Best Local Similarity 85.3%; Score 1087; DB 2; Length 232;

Matches 185; Conservative 22; Mismatches 18; Indels 0; Gaps 0;

Db

2 YGWMOSGATFTYGGDSAGTGMGACGYGNLYSGYGTNTVALSTALFNNGLSGACFEWT 61

7 YGWMESAHATFTYGGDSAGTGMGACGYGNLYSGYGTNTVALSTALFNNGLSGACFEWT 66

62 CTNDPKMCLPGTIRYATATNCPNFPALPNDGWCNPPLOHFDMAEPALQIAQYRAGIV 121

67 CNDPQWCLPGTYVTATNCPNFPALPNDGWCNPPLOHFDMAEPALQIAQYRAGIV 126

122 PVSEFRVPCMKKGGVFTINGHSYFNLYLTNVGAGDVHSVSIKSRGTGQMSRMWGQ 181

127 PLYTRVPCLRKGGIRFTVNGHSYFNLYLTNVGAGDVHVAHSIKSRSGWQPSRMWGQ 186

182 NMOSNNYLTNGGSLSFQVTLSDGRTLTAYNLVPSNMFGQTYEGPQ 226

187 NMOSNYLTNGGSLSFQVTLSDGRTVSNNAVPNMFGQTYEGSQ 231

RESULT 4

T09826

expansin (clone pteexp5) - loblolly pine (fragment)

C:Species: Pinus taeda (loblolly pine)

C>Date: 16-Jul-1999 #sequence-revision 16-Jul-1999 #text-change 26-May-2000

C:Accession: T09826

R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.

submitted to the EMBL Data Library, July 1996

A:Description: Expansins are conserved in conifers and expressed in response to exogenous

A:Reference number: Z16866

A:Accession: T09826

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-232 <HUT>

A:Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105

A:Experimental source: clone pteexp5

C:Superfamily: expansin

Query Match

Best Local Similarity 85.1%; Score 1085; DB 2; Length 232;

Matches 185; Conservative 23; Mismatches 17; Indels 0; Gaps 0;

Db

2 YGWMOSGATFTYGGDSAGTGMGACGYGNLYSGYGTNTVALSTALFNNGLSGACFEWT 61

7 YGWMESAHATFTYGGDSAGTGMGACGYGNLYSGYGTNTVALSTALFNNGLSGACFEWT 66

62 CTNDPKMCLPGTIRYATATNCPNFPALPNDGWCNPPLOHFDMAEPALQIAQYRAGIV 121

67 CNDPQWCLPGTYVTATNCPNFPALPNDGWCNPPLOHFDMAEPALQIAQYRAGIV 126

122 PVSEFRVPCMKKGGVFTINGHSYFNLYLTNVGAGDVHSVSIKSRGTGQMSRMWGQ 181

127 PLYTRVPCLRKGGIRFTVNGHSYFNLYLTNVGAGDVHVAHSIKSRSGWQPSRMWGQ 186

182 NMOSNNYLTNGGSLSFQVTLSDGRTLTAYNLVPSNMFGQTYEGPQ 226

187 NMOSNYLTNGGSLSFQVTLSDGRTVSNNAVPNMFGQTYEGSQ 231

RESULT 5

T09825

expansin (clone pteexp4) - loblolly pine (fragment)

C:Species: Pinus taeda (loblolly pine)

C>Date: 16-Jul-1999 #sequence-revision 16-Jul-1999 #text-change 26-May-2000

C:Accession: T09825

R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.

submitted to the EMBL Data Library, July 1996

A:Description: Expansins are conserved in conifers and expressed in response to exogenous

A:Reference number: Z16866

A:Accession: T09825

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-232 <HUT>

A:Cross-references: EMBL:U64892; NID:g1778102; PID:g1778103

A:Experimental source: clone pteexp4

C:Superfamily: expansin

Query Match

Best Local Similarity 84.5%; Score 1077; DB 2; Length 232;

Matches 183; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

Db

2 YGWMOSGATFTYGGDSAGTGMGACGYGNLYSGYGTNTVALSTALFNNGLSGACFEWT 61

7 YGWMESAHATFTYGGDSAGTGMGACGYGNLYSGYGTNTVALSTALFNNGLSGACFEWT 66

62 CTNDPKMCLPGTIRYATATNCPNFPALPNDGWCNPPLOHFDMAEPALQIAQYRAGIV 121

67 CNDPQWCLPGTYVTATNCPNFPALPNDGWCNPPLOHFDMAEPALQIAQYRAGIV 126

122 PVSEFRVPCMKKGGVFTINGHSYFNLYLTNVGAGDVHSVSIKSRGTGQMSRMWGQ 181

127 PLYTRVPCLRKGGIRFTVNGHSYFNLYLTNVGAGDVHVAHSIKSRSGWQPSRMWGQ 186

182 NMOSNNYLTNGGSLSFQVTLSDGRTLTAYNLVPSNMFGQTYEGPQ 226

187 NMOSNYLTNGGSLSFQVTLSDGRTVSNNAVPNMFGQTYEGSQ 231

Db 187 NMOSNYLNGQSLSFQVTTSDGRTVSNVAVPNSMNOFGOTFEGSQ 231

RESULT 6

FE4831

Probable expansin (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: FE4831

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKien, S.E.; Umayam, L.; Tallon, L.

enuss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: AB4420; MUID:20083487

A:Accession: FE4831

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <STO>

A:Cross-references: GB:AB02093; NID:92651297; PIDN:AB87577.1; GSPDB:GN00139

C:Genetics:

A:Gene: AT2G40610

A:Map position: 2

C:Superfamily: expansin

Query Match

Best Local Similarity 84.1%; Score 1072.5; DB 2; Length 253;

Matches 189; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

Db 1

QY 1 DYCGMOSGHATFYGGDASCTMGACGYGNLYSGGYGTNTVALSTALFNNGLSGACFEM 60

Db 26 DDGDMOGHATFYGGDASCTMGACGYGNLYSGGYGTNTVALSTALFNNGLSGACFEM 85

QY 61 TCTNDPKWCLPGTIRVTATNFCPPNFALPNDGGMCPNLPLOHMAEPALQIAYRAGI 120

Db 86 KCNDPDKWCLPGTIRVTATNFCPPNFALPNDGGMCPNLPLOHMAEPALQIAYRAGI 145

QY 121 VPVSFRVPCMKKGGVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRT-GMOSMRNW 179

Db 146 VPVSFRVPCMKKGGVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRT-GMOSMRNW 205

QY 180 GNMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGOTFEGPOF 227

Db 206 GNMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGOTFEGPOF 253

Db 206

RESULT 7

T04175

expansin - rice

C:Species: Oryza sativa (rice)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-May-2000

C:Accession: T04175

R:Cho, H.T.; Kende, H.

Plant Cell 9, 1661-1671, 1997

A:Title: Expression of expansin genes is correlated with growth in deepwater ce.

A:Reference number: Z15042; MUID:97480100

A:Accession: T04175

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-246 <CHO>

A:Cross-references: EMBL:U05246; NID:q1815680; PIDN:AA81662.1; PID:q1815681

A:Experimental source: cv. Pin Gaeu 56

C:Genetics:

A:Gene: EXP4

C:Superfamily: expansin

Query Match

Best Local Similarity 81.6%; Score 1041; DB 2; Length 246;

Matches 182; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 2

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Db 21 YCGMOSGHATFYGGDASCTMGACGYGNLYSGGYGTNTVALSTALFNNGLSGACFEM 80

Db 21

YCGMOSGHATFYGGDASCTMGACGYGNLYSGGYGTNTVALSTALFNNGLSGACFEM 80

Db 21

YCGMOSGHATFYGGDASCTMGACGYGNLYSGGYGTNTVALSTALFNNGLSGACFEM 80

Db 21

YCGMOSGHATFYGGDASCTMGACGYGNLYSGGYGTNTVALSTALFNNGLSGACFEM 80

Db 21

QY 62 CTNDPKWCLPGTIRVTATNFCPPNFALPNDGGMCPNLPLOHMAEPALQIAYRAGI 121

Db 81 CDNAGSSCLPGSITVTATNFCPPNFALPNDGGMCPNLPLOHMAEPALQIAYRAGI 140

QY 122 VPVSFRVPCMKKGGVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRTGMOSMRNW 181

Db 141 VPVSFRVPCMKKGGVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRTGMOSMRNW 200

QY 182 NMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGOTFEGPOF 227

Db 201 NMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGOTFEGPOF 246

QY 201

NMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGOTFEGPOF 246

Db 201

NMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGOTFEGPOF 246

Db 201

NMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGOTFEGPOF 246

Db 201

NMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGOTFEGPOF 246

Db 201

NMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGOTFEGPOF 246

Db 201

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Db 201

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Db 201

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Db 201

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Db 201

NMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGOTFEGPOF 246

Sun Oct 13 14:19:16 2002

us-09-896-301-7.rpr

Page 6

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Db      214 QNWQSNVILIGQSLSFRTASDRRSSTSWNVAPATWQFGQTFSGKNE 260
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Search completed: October 11, 2002, 15:01:01
Job time : 11.3919 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:54:05 ; Search time 8.87897 Seconds
(without alignments)
624.466 Million cell updates/sec

Title: US-09-896-301-7

Perfect score: 1275

Sequence: 1 DYGMQSGHATFYGGGDSAG.....AYNLVPSNMQFGQTYEGPQF 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1275	100.0	227	4	US-09-092-160-7
2	1021.5	80.1	226	2	US-08-440-517A-6
3	1021.5	80.1	226	4	US-09-092-160-6
4	1021	80.1	228	2	US-08-440-517A-2
5	1021	80.1	228	4	US-09-092-160-2
6	962	75.5	225	2	US-08-440-517A-5
7	962	75.5	225	4	US-09-092-160-5
8	857.5	67.3	222	2	US-08-440-517A-3
9	857.5	67.3	222	4	US-09-092-160-3
10	839	65.6	225	4	US-09-362-642-2
11	837	65.6	225	2	US-08-845-539-2
12	797	62.5	179	2	US-08-845-539-6
13	797	62.5	179	4	US-09-362-642-6
14	767.5	60.2	227	2	US-08-440-517A-4
15	767.5	60.2	227	4	US-09-092-160-4
16	732	57.4	167	2	US-09-362-642-4
17	732	57.4	167	4	US-08-845-539-4
18	245.5	19.3	261	1	US-07-971-096-2
19	245.5	19.3	261	1	US-08-175-096-2
20	233	18.3	246	4	US-08-441-507-21
21	231.5	18.2	263	1	US-07-971-096-4
22	231.5	18.2	263	1	US-08-175-096-4
23	231.5	18.2	263	4	US-08-413-974-6
24	231.5	18.2	263	4	US-08-434-418-6
25	231.5	18.2	263	4	US-08-433-288-6
26	231.5	18.2	263	4	US-08-174-739A-6
27	231	18.1	272	4	US-08-441-507-15

28	204	16.0	245	4	US-08-441-507-24	Sequence 24, Appl
29	173	13.6	197	4	US-08-441-507-5	Sequence 5, Appl
30	173	13.6	200	4	US-08-441-507-4	Sequence 4, Appl
31	139.5	10.9	122	4	US-08-441-507-23	Sequence 23, Appl
32	119.5	9.4	145	4	US-08-413-974-4	Sequence 4, Appl
33	119.5	9.4	145	4	US-08-434-418-4	Sequence 4, Appl
34	119.5	9.4	145	4	US-08-433-288-4	Sequence 4, Appl
35	119.5	9.4	145	4	US-08-174-739A-4	Sequence 4, Appl
36	100.5	7.9	54	3	US-08-750-419A-12	Sequence 12, Appl
37	95.5	7.5	145	4	US-08-441-507-16	Sequence 16, Appl
38	93.5	7.3	145	4	US-08-441-507-2	Sequence 2, Appl
39	86.5	6.8	138	4	US-08-441-507-7	Sequence 7, Appl
40	84.5	6.6	633	3	US-09-041-991A-8	Sequence 8, Appl
41	84.5	6.6	633	3	US-09-041-991A-10	Sequence 10, Appl
42	81.5	6.4	402	2	US-08-491-988-9	Sequence 9, Appl
43	79	6.2	402	1	US-08-460-806-11	Sequence 11, Appl
44	79	6.2	402	1	US-08-325-630-11	Sequence 11, Appl
45	78.5	6.2	418	4	US-09-254-733-5	Sequence 5, Appl

ALIGNMENTS

```
RESULT 1
US-09-092-160-7
: Sequence 7, Application US/09092160C
: Patent No. 6255466
: GENERAL INFORMATION:
: APPLICANT: Cosgrove, Daniel J
: APPLICANT: McQueen-Mason, Simon
: APPLICANT: Guiltinan, Mark J
: APPLICANT: Shcherban, Tatyana
: APPLICANT: Shi, Jun
: TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
: FILE REFERENCE: 1194/1C114053
: CURRENT APPLICATION NUMBER: US/09/092,160C
: EARLIER FILING DATE: 1998-06-05
: EARLIER APPLICATION NUMBER: 08/440,517
: EARLIER FILING DATE: 1995-05-12
: EARLIER APPLICATION NUMBER: 08/242,090
: EARLIER FILING DATE: 1994-05-12
: EARLIER APPLICATION NUMBER: 08/060,944
: EARLIER FILING DATE: 1993-05-12
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 227
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: cucumber
: OTHER INFORMATION: expansin
US-09-092-160-7

Query Match          100.0%; Score 1275; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DYGMQSGHATFYGGGDSAGTGMGACGYGNTYSGYGTNTVALSTPALFNNGLSGCGACHEM 60
DB 1 DYGMQSGHATFYGGGDSAGTGMGACGYGNTYSGYGTNTVALSTPALFNNGLSGCGACHEM 60
QY 1 TCTNDPKKCLGTTTAVTATNCPNFALPNDGMCNPLQHPMAEPFLQIOYRAGT 120
DB 1 TCTNDPKKCLGTTTAVTATNCPNFALPNDGMCNPLQHPMAEPFLQIOYRAGT 120
QY 121 VVPSFRVPCMKKGGVRETTINGHSYFNLVLTNNVGAGADVSVSIKGSRTGWSMNRWG 180
DB 121 VVPSFRVPCMKKGGVRETTINGHSYFNLVLTNNVGAGADVSVSIKGSRTGWSMNRWG 180
QY 181 QNMOSNNLNQGLSFOVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 227
DB 181 QNMOSNNLNQGLSFOVTLSDGRTLTAYNLVPSNMQFGQTYEGPQF 227

Best Local Similarity 78.8%; Pred. No. 2.6e-93;
Matches 175; Conservative 23; Mismatches 24; Indels 0; Gaps 0;

[illegible]

RESULT 5
US-09-092-160-2

OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160-2

Query Match	80.1%, Best Local Similarity	Score 1021, Pred. No. 2,6e-93	DB 4:	Length 228:
Matches 175:	Conservative 23:	Mismatches 24:	Indels 0:	Gaps 0:
Qy 3 GGMGGHATFFYGGGASGTCMGACGCGYNNYSOGYSTNNVALSTALFENNGISGCAFEETMC				
Db 3 GGMVNAHATFTYGGGASGTCMGACGCGYNNYSOGYSTNNVALSTALFENNGISGCAFEETRC				
Qy 63 TNDPMKCLPCTTIRVATATNEFCNPENALPNDGDCNPLQHEFMAEPALQIAQYRAGIYV				
Db 63 QNDGKWCMLPGSIVYVATATNEFCNPENNALPNWAGGWCNRPDQHPLDSQPVFORIAQYRAGIYV				
Qy 123 VERRPVCMKKGGVFTTNGHSYFNLYLTITNGGAGDYVSIKTSRPTGQMSNRMGON				
Db 123 VARRPVCARRGGIRFTTNGHSYFNLYLTITNGGAGDYVSAWVKSRPTGQMSNRMGON				
Qy 183 WQSNNTVLNGQGLSFQVLTLDGRTLTVAYNLVPSNMQFGQTYEG				
Db 183 WQSNNTVLNGQGLSFQVLTLDGRTLTVAYNLVPSNMQFGQTYEG				

RESULT 6
US-08-440-517A-5

Query Match	75.58;	Score 962;	DB 2;	Length 11	225;
Best Local Similarity	75.08;	Pred. No. 1.7e-87;			
Matches 171; Conservative	26;	Mismatches 27;	Indels	4;	Gaps 2;

[illegible]

RESULT 7
 US-09-092-160-5
 Sequence 5, Application US/0902160C
 Patent No. 6255466
 GENERAL INFORMATION:
 APPLICANT: Cosgrove, Daniel J
 APPLICANT: McQueen-Mason, Simon
 APPLICANT: Gullinan, Mark J
 APPLICANT: Sheherban, Tatyana
 APPLICANT: Shi, Jun
 TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 FILE REFERENCE: 1194/1C114US3
 CURRENT APPLICATION NUMBER: US/09/092.160C
 CURRENT FILING DATE: 1998-06-05
 EARLIER APPLICATION NUMBER: 08/440,517

EARLIER FILING DATE: 1995-05-12
 EARLIER APPLICATION NUMBER: 08/242,090
 EARLIER FILING DATE: 1994-05-12
 EARLIER APPLICATION NUMBER: 08/060,944
 EARLIER FILING DATE: 1993-05-12
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5
 LENGTH: 225
 TYPE: PRF
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
 OTHER INFORMATION: expansin
 US-09-092-160-5

Query Match 75.5%; Score 962; DB 4; Length 225;
 Best Local Similarity 75.0%; Pred. No. 1,7e-87;
 Matches 171; Conservative 26; Mismatches 27; Indels 4; Gaps 2;

QY 1 DYGGQSGHATFYGGGASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEM 60
 Db 1 DNGWGERHATFYGGADSGTMGACGYNLYSGYGTNTVALSTALFNSQKCGACFEL 60
 QY 61 TCTNDPKWCLPGTIRVTATNFCPPNFALPNDGCMCNPLQHFMAPEAFLOIAQYRAGI 120
 Db 61 TCEDDEKCIPIRGSIIV--RYNLANFALANDNGCMCNPLKHFPLAPFLQIAQYRAGI 117
 QY 121 PVSFRRVPCMKKGGVFTINGHSYFNLYLTITNGAGADVHSVSIKSRFG-WQMSRNN 179
 Db 118 VPVAFRRVPCKEGGIRFTINGSNPYFDLIVLTITNGAGADIRAVSLKSKTDOMQMSRNN 177
 QY 180 GNMOSNNYLLNGGSLSFQVLTSDGRTLTAVNLVPSNMQFGQTYEGPOF 227
 Db 178 GNMOSNNYLLNGGSLSFQVLTSDGRTVSVIDVPHDMQFGQTYEGPOF 225

RESULT 8
 US-08-440-517A-3
 Sequence 3, Application US/08440517A
 Patent No. 595082
 GENERAL INFORMATION:
 APPLICANT: COSGROVE, DANIEL J.;
 APPLICANT: GULLINAN, MARK;
 APPLICANT: SHERBAN, TATYANA;
 APPLICANT: SHI, JUN
 TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
 ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
 STREET: 113 TECHNOLOGY CENTER
 CITY: UNIVERSITY PARK
 STATE: PENNSYLVANIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 16802-7000
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: NEC 286
 OPERATING SYSTEM: DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/440,517A
 FILING DATE:
 CLASSIFICATION: 530
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 222
 TYPE: AMINO ACID
 TOPOLOGY: UNKNOWN
 US-08-440-517A-3

Query Match 67.3%; Score 857.5; DB 2; Length 222;

Best Local Similarity 67.3%; Pred. No. 3.6e-77;
 Matches 152; Conservative 26; Mismatches 39; Indels 9; Gaps 2;

QY 3 GGMQSGHATFYGGGASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEMTC 62
 Db 3 GPMINAHATFYXXGDXXTMGACGYNLYSGYGTNTVALSTALFDGSLGACXELMC 62
 QY 63 TNDPKWCLPG-TIRVTATNFCPPNFALPNDGCMCNPLQHFMAPEAFLOIAQYRAGI 121
 Db 63 VNDPQWCIKGRSIVVTATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
 QY 122 PVSFRRVPCMKKGGVFTINGHSYFNLYLTITNGAGADVHSVSIKSRFGWQMSRNNQ 181
 Db 115 PVMYRRVRCKRSGGIRFTINGHSYFNLYLTITNGAGADVHSVSMKSRITKQMLMSRNNQ 174
 QY 182 NMOSNNYLLNGGSLSFQVLTSDGRTLTAVNLVPSNMQFGQTYEGPOF 227
 Db 175 NMOSNNYLLNGGSLSFVLTSDGRTVSVVAPPTWSFGQTYEGPOF 220

RESULT 9
 US-09-092-160-3
 Sequence 3, Application US/09092160C
 Patent No. 625466
 GENERAL INFORMATION:
 APPLICANT: Cosgrove, Daniel J
 APPLICANT: McQueen-Mason, Simon
 APPLICANT: Gullinan, Mark J
 APPLICANT: Sherban, Tatyana
 APPLICANT: Shi, Jun
 TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 FILE REFERENCE: 1194/1C14US3
 CURRENT APPLICATION NUMBER: US/09/092,160C
 CURRENT FILING DATE: 1998-06-05
 EARLIER APPLICATION NUMBER: 08/440,517
 EARLIER FILING DATE: 1995-05-12
 EARLIER APPLICATION NUMBER: 08/242,090
 EARLIER FILING DATE: 1994-05-12
 EARLIER APPLICATION NUMBER: 08/060,944
 EARLIER FILING DATE: 1993-05-12
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 222
 TYPE: PRF
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: rice expansin
 NAME/KEY: UNSURE
 LOCATION: (14)-(58)
 OTHER INFORMATION: Xaa is unknown or other.
 US-09-092-160-3

Query Match 67.3%; Score 857.5; DB 4; Length 222;
 Best Local Similarity 67.3%; Pred. No. 3.6e-77;
 Matches 152; Conservative 26; Mismatches 39; Indels 9; Gaps 2;

QY 3 GGMQSGHATFYGGGASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEMTC 62
 Db 3 GPMINAHATFYXXGDXXTMGACGYNLYSGYGTNTVALSTALFDGSLGACXELMC 62
 QY 63 TNDPKWCLPG-TIRVTATNFCPPNFALPNDGCMCNPLQHFMAPEAFLOIAQYRAGI 121
 Db 63 VNDPQWCIKGRSIVVTATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
 QY 122 PVSFRRVPCMKKGGVFTINGHSYFNLYLTITNGAGADVHSVSIKSRFGWQMSRNNQ 181
 Db 115 PVMYRRVRCKRSGGIRFTINGHSYFNLYLTITNGAGADVHSVSMKSRITKQMLMSRNNQ 174
 QY 182 NMOSNNYLLNGGSLSFQVLTSDGRTLTAVNLVPSNMQFGQTYEGPOF 227
 Db 175 NMOSNNYLLNGGSLSFVLTSDGRTVSVVAPPTWSFGQTYEGPOF 220

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RESULT 10
US-09-362-642-2
; Sequence 2, Application US/09362642
; Patent No. 6350935
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
; FILE REFERENCE: 023070-078210US
; CURRENT APPLICATION NUMBER: US/09/362,642
; CURRENT FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum cv. T5

Query Match
Best Local Similarity 74.7%; Score 839; DB 4; Length 225;
Matches 145; Conservative 21; Mismatches 24; Indels 4; Gaps 2;

QY 3 GGMOSGHAATFYGGDASCTMGACGYNLYSQGYGTNTALSTALFNNGLSGACFEWTC 62
Db 31 GSWETAHATFYGGSDASCTMGACGYNLYSQGYGTNTALSTALFNNGLSGACFEWTC 62
QY 63 TNDP--KWCLPG--TIVTATNFCPPNFPALPNDGCMCPPLQHFDMAPFLQIAQYRA 118
Db 91 TNPMMKCLPGNPSILITATNFCPPNFPALPNDGCMCPPLQHFDMAPFLQIAQYRA 150
QY 119 GIVPVSFRVPCMKKGGVFTNGHSYFNLYLTNNVGAGDVHSVTSKGRSTGQMSRN 178
Db 151 GIVPVTTRIRPCRKGGIRFTNGFRFNLYLTNNVAGADITKVVWKGKTKTMIALSRN 210
QY 179 WGMQMSNNTLNGQ 192
Db 211 WGMQMSNAVLTLGQ 224

RESULT 11
US-08-845-539-2
; Sequence 2, Application US/08845539
; Patent No. 5929303
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,539
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774

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; REFERENCE/DOCKET NUMBER: 023070-078200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-845-539-2

Query Match
Best Local Similarity 74.7%; Score 837; DB 2; Length 225;
Matches 145; Conservative 20; Mismatches 25; Indels 4; Gaps 2;

QY 3 GGMOSGHAATFYGGDASCTMGACGYNLYSQGYGTNTALSTALFNNGLSGACFEWTC 62
Db 31 GSWETAHATFYGGSDASCTMGACGYNLYSQGYGTNTALSTALFNNGLSGACFEWTC 62
QY 63 TNDP--KWCLPG--TIVTATNFCPPNFPALPNDGCMCPPLQHFDMAPFLQIAQYRA 118
Db 91 TNPMMKCLPGNPSILITATNFCPPNFPALPNDGCMCPPLQHFDMAPFLQIAQYRA 150
QY 119 GIVPVSFRVPCMKKGGVFTNGHSYFNLYLTNNVGAGDVHSVTSKGRSTGQMSRN 178
Db 151 GIVPVTTRIRPCRKGGIRFTNGFRFNLYLTNNVAGADITKVVWKGKTKTMIALSRN 210
QY 179 WGMQMSNNTLNGQ 192
Db 211 WGMQMSNAVLTLGQ 224

RESULT 12
US-08-845-539-6
; Sequence 6, Application US/08845539
; Patent No. 5929303
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,539
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-078200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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US-08-845-539-6

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Query Match	62.58;	Score 797;	DB 2;	Length 179;
Best Local Similarity	79.18;	Pred. No. 2.6e-71;		
Matches 140;	Conservative 13;	Mismatches 22;	Indels 2;	Gaps 1.

Qy	10	ATPFGGGDASTGTMGACGCGYKLTSSQGGTNTVALSTALFNNGLSSCGAFCEMTLCLNPNMC	6
Db	3	ATPFGGSDASTGTMGACGCGYKLTSSQGGTNTALSTALFNNGLSSCGAFCEIKCANDBRMC	62
Qy	70	LPGT - -TRVATNCPENFALPNDDGMCNPRLOHPHMAEPALQIAYRAGIVPYSFR	127
Db	63	HPSPCFITATNCPENFALPNDDGMCNPRHPHFLDAMEFLKIEYRAGIDTPYSYR	122
Qy	128	VPCAKKGAVRTINGHSYFNLYLTTNNGGADYVSTSSCGRTQWQSMRMGQNMQ	184
Db	123	VPCRKGGIRFTINGFRFNLYLTTNNAAGADIVRYEVSKGNTGQMSMRMGQNMQ	179

RESULT 13
US-09-362-642-6
; Sequence 6, Application US/09362642

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: Patent NO.6350935
: GENERAL INFORMATION:
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: APPLICANT: Bennett, Alan B.
: APPLICANT: Rose, Jocelyn K.C.
: APPLICANT: The Regents of the University of California
: TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
: TITLE OF INVENTION: to Control Fruit Texture and Softening
: FILE REFERENCE: 023070-078210US
: CURRENT APPLICATION NUMBER: US/09/362,642
: CURRENT FILING DATE: 1999-07-27
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: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: Patentln Ver. 2.1
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: LENGTH: 179
: TYPE: prf
: ORGANISM: Cucumis melo
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: US-09-362-642-6

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Query Match          62.5%; Score 797; DB 4; Length 179;
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        ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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QY      128 VPCMKKGVRFTINGISTRNLYLITRVGVGAGDVHASYISGSRFNGSMSNRMNGCMMO 184
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DB       123 VPCRKGGIGRTITNGRYENLVLTITNVAGADIVRVSVKGSNTGMSNRHMNQMMO 179

RESULT 14
US-08-440-517A-4
; Sequence 4, Application US/08440517A
; Patent No. 5959082
; GENERAL INFORMATION:
; APPLICANT: COSGROVE, DANIEL J.;
; APPLICANT: GUTTMAN, MARK;
; APPLICANT: SHERBAN, TATIANA;
; APPLICANT: SHI, JUN
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
; ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: PENNSYLVANIA PARK
; STATE: PENNSYLVANIA

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1  COUNTRY:  UNITED STATES OF AMERICA
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3  ZIP:  16802-7000
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7  MEDIUM TYPE:  FLOPPY DISK
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9  COMPUTER:  NEC 286
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11 OPERATING SYSTEM:  DOS
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13 SOFTWARE:  WORDPERFECT 5.1
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15 CURRENT APPLICATION DATA:
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17 APPLICATION NUMBER:  US/08/440,517A
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19 FILING DATE:
20
21 CLASSIFICATION:  530
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23 INFORMATION FOR SEQ ID NO: 4:
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25 SEQUENCE CHARACTERISTICS:
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27     LENGTH:  227
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29     TYPE:  AMINO ACID
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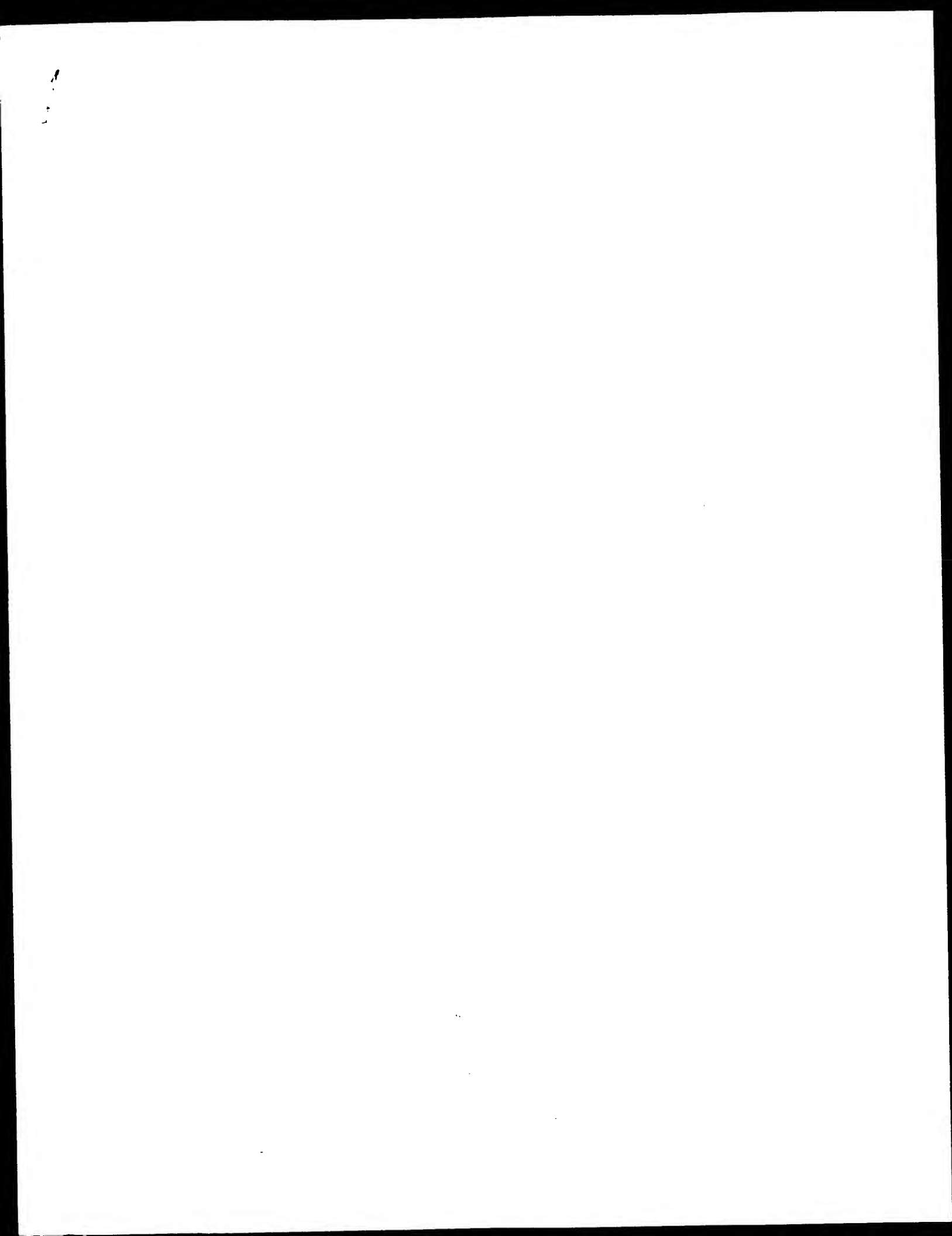
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RESULT 15 160-4
US-09-092-160-4
; Sequence 4, Application US/09092160C
; Patent No. 6255466
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Guilleman, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/1C114US3
; CURRENT APPLICATION NUMBER: US/09/092,160C
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 08/440,517
; EARLIER FILING DATE: 1995-05-12
; EARLIER APPLICATION NUMBER: 08/242,090
; EARLIER FILING DATE: 1994-05-12
; EARLIER APPLICATION NUMBER: 08/060,944
; EARLIER FILING DATE: 1993-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
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; NAME/KEY: UNSURE
; LOCATION: (2)..(227)
; OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160-4

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Query Match 60.2%; Score 767.5; DB 4; Length 227;
Best Local Similarity 64.0%; Pred No. 2.9e-68;
Matches 137; Conservative 27; Mismatches 47; Indels 3; Gaps 2;
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QY 65 DPKWCLPG--TTRVTATNFCPPNFALPNDGMCNPLQHFDMAPFLQIAQYRAGIYP 122
DB 66 QTRKCKPFGNSITTTATNLCPNMAALPSNSGMCNPLXHPDMSQPAWENIAVYQAGIYP 125
QY 123 VSEFRVPCMKKGVRFTINGHSYFNLVLTNVGAGADVHSYIKSRTGMQMSRNMGN 182
DB 126 VNYKRVXPORSRGIRFALISGHDFELVYVTNVGSGCYVAQMSIKSNTGMWMSRNMGN 185
QY 183 WQSNMYLNGOGLSFQVTLSDGRTLTAIYLVPSNW 216
DB 186 WQSNATYLAGQSLSFIVQLDDGRKRYTAMNXPXNW 219

Search completed: October 11, 2002, 15:02:08
Job time : 9.87897 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:49:55 : Search time 25.1292 Seconds
(without alignments)
1003.367 Million cell updates/sec

Title: US-09-896-301-7

Perfect score: 1275

Sequence: 1 DYCGMGSHATFYCGDASG.....AYNLVPSNMQFGQTYEGSPQF 227

Scoring table:

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Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1072.5	84.1	253	21	AMG46483
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7	1031	80.9	249	21	AMG06545
8	1031	80.9	249	21	AMG51632
9	1031	80.9	249	21	AMG51646
10	1031	80.9	259	21	AMG06544
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12	1031	80.9	280	21	AMG51645	Arabidopsis thalia
13	1021	80.1	228	17	AR94528	Rice expansin, Or
14	1019	79.9	251	21	AMG23852	Arabidopsis thalia
15	1019	79.9	251	21	AMG43343	Arabidopsis thalia
16	1019	79.9	253	21	AMG23851	Arabidopsis thalia
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20	1012.5	79.4	227	17	AR94532	Arabidopsis thalia
21	985	78.0	250	22	AMG00414	Tomato seed expans
22	984	77.3	257	21	AMG36445	Arabidopsis thalia
23	970.5	76.1	207	21	AMG25444	Arabidopsis thalia
24	970.5	76.1	207	21	AMG46484	Arabidopsis thalia
25	965	75.7	249	21	AMG05452	Arabidopsis thalia
26	965	75.7	249	21	AMG05453	Arabidopsis thalia
27	962	75.5	225	17	AMG94531	Arabidopsis thalia
28	962	75.5	225	17	AMG36570	Arabidopsis thalia
29	960	75.3	242	21	AMG36569	Arabidopsis thalia
30	960	75.3	249	21	AMG36568	Arabidopsis thalia
31	960	74.8	252	21	AMG29931	Arabidopsis thalia
32	954	74.8	273	21	AMG29930	Arabidopsis thalia
33	954	73.6	255	21	AMG30325	Arabidopsis thalia
34	939	73.6	257	21	AMG30324	Arabidopsis thalia
35	939	73.6	253	22	AMG00412	Arabidopsis thalia
36	934	73.3	250	21	AMG09622	Tomato seed expans
37	934	73.3	258	21	AMG09621	Arabidopsis thalia
38	934	73.3	280	21	AMG09620	Arabidopsis thalia
39	895	70.2	210	21	AMG36446	Arabidopsis thalia
40	889.5	69.8	221	21	AMG15694	Arabidopsis thalia
41	889.5	69.8	221	21	AMG51013	Arabidopsis thalia
42	889.5	69.8	225	21	AMG13693	Arabidopsis thalia
43	889.5	69.8	225	21	AMG51012	Arabidopsis thalia
44	889.5	69.8	225	21	AMG29932	Arabidopsis thalia
45	866	67.9	210	21		

ALIGNMENTS

RESULT 1
AAR94527 standard; Protein; 227 AA.
XX
AC AAR94527;
XX
DT 08-JUL-1996 (first entry)
XX
DE Cucurbit expansin-29.
XX
KW Cucurbit expansin-29; plant cell wall; cellulose; paper recycling; de-linking;
XX polysaccharide; cucumber.
OS Cucumis sativus var. Burpee Pickler.
XX
PN AU9540262-A.
XX
PD 04-APR-1996.
XX
PF 12-MAY-1994; 94AU-0068320.
XX
PR 12-MAY-1995; 95US-0440517.
XX
PR 12-MAY-1993; 93US-0060944.
XX
PA (PENN-) PENN STATE RRS FOUND.
XX
PI Cosgrove DJ, McQueen-Mason S;
XX WPI. 1996-201150/21.
XX N-PSDB; AAT13320.
XX
PT Expansin proteins which alter the mechanical strength of
XX poly:saccharide(s) - useful in paper mfr. and recycling


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PR 21-JUL-1999; 99US-0145086.
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Query Match 84.1%; Score 1072.5; DB 21; Length 253;
 Best Local Similarity 82.9%; Pred. No. 3.7e-100;
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DB 86 KCNDPRMCLGSTITVTATNFCPPNPLSLNDGCMCPPIQIDMAPLQIAOVRAGI 145
QY 121 VPSFRRVPCMKKGVRFTINGHSYFNLVLTIVGAGDVHSYSIKSRT-GMOSMRW 179
DB 146 VPSFRRVPCMKKGIFFTINGHSYFNLVLSNVGAGDVHAYSINGSKTSQMSMRW 205
QY 180 GOMNOSNYLNGGLSFOVTLSDGRTLTATNVLPSMNOFCQTEGQOF 227
DB 206 GOMNOSNYLNGGLSFOVTLSDGRTLTATNVLPSMNOFCQTEGQOF 253

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RESULT 3
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ID AAC6483 standard; protein; 253 AA.
XX
AC AAC6483;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58485.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; protein;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN
XX
PD EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Query Match 84.1%; Score 1072.5; DB 21; Length 253;
Best Local Similarity 82.9%; Pred. No. 3.7e-100;
Matches 189; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

OY 1 DYGGNQGSHAFYGGGDSGTMGACGCGNLSQCTGNTVATLSTALFNNGISGACPEM 60
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DB 146 VPSFRARVPCKKGGVARTINGHSYFNLVLTNNGACDVHSVSTIKGSR- GWOSSMRNW 205
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RESULT 4
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AC AAG06546;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 3357.

KM Protein identification: signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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Protein identification: signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;

termination sequence.
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Query Match 80.9%; Score 1031; DB 21; Length 249;
Best Local Similarity 78.7%; Pred. No. 5, 7e-96;
Matches 177; Conservative 25; Mismatches 23; Indels 0; Gaps 0;

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OY 63 TNDPKWCLPGLTAVTATNFCPPNFALPNDGNCNPPLOHEDNAEPALQIAOYRAGIYP 122
DB 84 ENDGKRCPLGSIYVATNFCPPNFALPNDGNCNPPLOHEDNAEPALQIAOYRAGIYP 143
OY 123 VSEFRPCKKKGVFTTNGHSYFNVLVTNNGGACDVHSVSKSGSTQGSRRMNGON 162
DB 144 VSYRVPCKRRRGIRFTNGHSYFNVLVTNNGGACDVHSVSKSGSTQGSRRMNGON 203
OY 183 WQSNNTLNGQSLFQYTLSDGRTLVAVNLVPSNMOPGQTEGPOF 227
DB 204 WQSNNTLNGQSLFQYTLSDGRTLVAVNLVPSNMOPGQTEGPOF 248

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DT 18-OCT-2000 (first entry)

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Query Match	80.9%;	Score 1031;	DB 21;	Length 249;
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XX AAG51646;
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XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 65569.
DE
XX Arabidopsis thaliana protein fragment SEQ ID NO: 65569.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS
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Query Match 80.9%; Score 1031; DB 21; Length 249;
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
PN EPI033405-A2.
PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
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XX Protein identification: signal transduction pathway; metabolic pathway;
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OS Arabidopsis thaliana.
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RESULT 13
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AC AAR94528;
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XX 08-JUL-1996 (first entry)
DE
XX Rice expansin.
XX Expansin: plant cell wall; cellulose; paper recycling; de-linking;
XX polysaccharide; rice.
XX
XX Oryza sativa.
XX
XX Key Location/Qualifiers
XX MISC-difference 211
XX /note= "unidentified amino acid"
XX
XX A09540262-A.
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XX 12-MAY-1995; 95US-0440517.
XX 12-MAY-1993; 93US-0060944.
XX
XX (PENN-) PENN STATE RES FOUND.
XX
XX Cosgrove DJ, McQueen-Mason S;
XX
XX WPI: 1996-201150/21.
XX
XX Expansin proteins which alter the mechanical strength of
XX polysaccharide(s) - useful in paper mfr. and recycling
XX
XX Disclosure: Page 30-31; 60pp; English.
XX
XX Expansins are a novel class of proteins that catalyze the extension
XX of plant cell walls and the weakening of the hydrogen bonds in pure
XX cellulose. 2 Expansins (AAR94528 and AAR94529) have been identified in
XX rice and 3 in Arabidopsis (AAR94530-33). A cDNA clone (AAT13320)
XX coding for cucumber expansin 29 (AAR94527) has been obtd. Expansins
XX can be used e.g. in the mfr. de-linking and recycling of paper, in
XX the textile industry, to aid delignification processes, to alter gel
XX mechanical strength, etc.
XX
XX Sequence 228 AA:
XX
Query Match 80.1%; Score 1021; DB 17; Length 228;
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AC AAG23852;
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XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 27311.
XX
XX Protein identification: signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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XX Arabidopsis thaliana.
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XX EP1033405-A2.
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XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 13-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 18-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 79.9%; Score 1019; DB 21; Length 251;
Best Local Similarity 77.7%; Pred. No. 9; 4e-95;
Matches 174; Conservative 24; Mismatches 26; Indels 0; Gaps 0;

QY 4 GMSGHATFYGGDASGTMGACGYGMLYSOGYGTNTVALSTALPNNGLSCGACFEMTCT 63
DB 27 GVNNAHATFYGSDASGTMGACGYGMLYSOGYGTNTALSTALPNNGLSCGACFEIKCO 86
QY 64 NDPKWCLEPRTIRVATNCPNFPALPNDGAGCNPLQHFDMAPAFLOIAQYRAGIVPV 123
DB 87 SDGAWCLFCAITVATNCPNNAIPNNAGGWCNPLHNFEDLSQPVFORIAQYKAGIVPV 146
QY 124 SFRVPCMKKGGVREFTINGHSYFNLVLTIVNGAGDVHSINGSRIGMSMRNNGCON 183
DB 147 SYRVPCKMRGGIRFTINGHSYFNLVLTIVNGAGDVHSVAVKSRTRWOOMSRNNGCON 206
QY 184 OSNNYLNCGISFOYVLSGRTLAAYNLVPSNMQFGOTYEGPOF 227
DB 207 OSNNLNGQALSFKVYASDGRIVSNNTIAPASMSFGOTFTGRCP 250

Search completed: October 11, 2002, 14:56:45
Job time : 26.1292 secs

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RESULT 7
MPOL_ORYSA STANDARD; PRT: 263 AA.
ID AC
MP01 ORSA 040638: 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Major pollen allergen Ory s 1 precursor (Ory s I).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Anther;
RX MEDLINE=96069591; PubMed=7590339;
RA Xu H., Theerakulpisut P., Goulding N., Suphioglu C., Singh M.B.,
RT "Cloning, expression and immunological characterization of Ory s 1,
RL the major allergen of rice pollen."
CC Gene 164:255-259(1995).
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: EXPRESSED IN MATURE ANTHERS BUT NOT IN
CC VEGETATIVE OR OTHER FLORAL TISSUES.
CC - DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC - SIMILARITY: BELONGS TO THE LOI P I FAMILY OF ALLERGENS.
CC - SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC - SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
-----
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-----
CC EMBL: U31771; AAA86533.1; -.
CC HSSP: PA4314; WHO.
DR InterPro: IPRO00882; Pollen.allergen.
DR Pfam: PF01357; Pollen.allergen. 1.
DR PRINTS: PR01225; EXPANSNFRMLX.
DR ProDom: PD002179; Pollen.allergen. 1.
DR PROSITE: PS50843; EXPANSIN_CBD. 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 263 MAJOR POLLEN ALLERGEN ORY S 1.
FT DOMAIN 61 164 EXPANSIN-LIKE EG45.
FT DOMAIN 178 259 EXPANSIN-LIKE CBD.
FT CARBOHD 32 32 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 263 AA; 28497 MW; BIC524EA338DD60 CRC4;
Query Match 17.4%; Score 216.5; DB 1; Length 263;
Best Local Similarity 27.4%; Pred. No. 2,3e-12;
Matches 55; Conservative 39; Mismatches 82; Indels 25; Gaps 7
OY 23 GSAGCGYNLIHSQGYLGQTALSTALFNSGCKGACFELTCDDDEWCIPIGSIIYRYMIAN 82
DB 61 GGACGKYVDKAPFLGMNSCGNDPFKKGGKGSCFEIKC-SKEPACSDRKALLHYDMN 119
OY 83 PALANDNGWCMPPLK--HFDLAEPAFLDIAQ---YAGIYPVAFFRVPCSGGGIRFT 136
DB 120 -----DEPLAIHYFDLSGLAMAKDKDELBRAGIIDTFRRVVKCKYPADTKIT 168
OY 137 IN--GNPYFDVLITLVNGAGADIRAVSLKSKTDOMQSMRMNQMWQSNLT--YLNGQ 190
DB 169 FHEIKASNNRYIALLYKVAYGDGDVEYEIKEGSGEWMALKESGAIMRIDTPKLKG- 227
OY 191 SLSEFYATDSDGRTIVSYDYVP 211

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Db      228 PFSVRVTEGARRSSAEDAIP 248

RESULT 8
GUNS_TIRE STANDARD; PRT; 242 AA.
ID GUNS_TIRE
AC P4317;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)
DE (Cellulase V) (EG V).
GN EG45.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-QM9414 / RUT C-30;
RX MEDLINE=95075308; Pubmed=7984103;
RA Salohelmo A., Henttisaari B., Hoffman A.-M., Teleman O., Penttilä M.;
RT "A novel, small endoglucanase gene, eg15, from Trichoderma reesei
   isolated by expression in yeast."
RL Mol. Microbiol. 13:219-226(1994).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
   linkages in cellulose.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY K (FAMILY 45 OF GLYCOSYL
   HYDROLASES).
CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
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   or send an email to licenses@isb-sib.ch).
CC -----
DR EMBL: Z33381; CAA83846.1; .
DR HSPB: P00725; 2CBH.
DR InterPro: IPR000254; CBD_fungal.
DR InterPro: IPR000334; Glyco_hydro_45.
DR Pfam: PF00734; CBD_1.1.
DR Pfam: PF02015; Glyco_hydro_45; 1.
DR ProDom: PD001821; CBD_fungal; 1.
DR SMART: SM00236; fcbd; 1.
DR PROSITE: PS00562; CBD_FUNGAL; 1.
DR PROSITE: PSS0842; EXPANSIN_EH45; 1.
DR PROSITE: PS01140; GLYCOSYL_HYDROL_F45; 1.
DR Cellulose degradation: Hydrolase; Glucosidase; Signal.
KW SIGNAL
FT CHAIN 1 242
FT ACT_SITE 27 27 ENDOGLUCANASE V.
FT ACT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
FT DOMAIN 18 182 PROTON DONOR (BY SIMILARITY).
FT DOMAIN 183 205 CATALYTIC.
FT DOMAIN 206 242 PRO/SER-RICH (LINKER).
FT CARBOHD 182 182 CELLULOSE-BINDING (BY SIMILARITY).
FT DISULFD 213 230 N-LINKED (GLCNAC.. ) (POTENTIAL).
FT DISULFD 224 240 BY SIMILARITY.
FT SEQUENCE 242 AA; 2441 MW; CC033FC51326C71D CRC64;

Query Match 8.0%; Score 99; DB 1; Length 242;
Best Local Similarity 30.4%; Pred. No. 0.067;
Matches 38; Conservative 11; Mismatches 28; Indels 48; Gaps 9

QY 12 FYGGADASTMGAGCYGMTHSQ-----GYGLOTATLTALFNPS-----GQKCGACF 58
   : : : : | | | | : : : : : : : : : : : : : : : : : : : : : :
DB 25 YVDGE-----GACGCGSSGAFPMWLGIGNGVTTAAGSALPDFTAASGAGCGCKY 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 59 ELT-----CEDPEWCIPG-----SIIVRYLANFALANDNGWCPNL----- 97
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 5
MPC1 CYA

ID	NAME	STANDARD	PRT	AA
AC	MPC1_CYNDA			246
AD	004701			
DT	16-Oct-2001	(Rel. 40, Created)		
DT	16-Oct-2001	(Rel. 40, Last sequence update)		
DT	01-MAR-2002	(Rel. 41, Last annotation update)		
DE	Major pollen allergen Cyn d 1.			
GN	CYNDA1.			
OS	Cynodon dactylon (Bermuda grass).			
OC	Eukaryota: Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;			
OC	Spermatophytes, Mesangiosperms, Liliopsida, Poales; Poaceae; PACC clade,			
OC	Chloridoideae; Cynodonteae; Cynodon.			
OX	NCBI_TaxID=28909;			
TX	111			

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-Pollen;
RX MEDLINE=96347957; PubMed=8757211;
RA Smith P.M., Supphloglo C., Griffith I.J., Theriault K., Knox R.B.,
RA Singh M.B.;
RT "Cloning and expression in yeast *Pichia pastoris* of a biologically
RT active form of Cyn d 1, the major allergen of Bermuda grass pollen.";
RL J. Allergy Clin. Immunol. 98:331-343(1996).
CC -
CC - SUBCELLULAR LOCATION: Secreted.
CC -
CC - DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -
CC - SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
CC -
CC - SIMILARITY: CONTAINS 1 EXPANSIN-LIKE BG45 DOMAIN.
CC -
CC - SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
CC -----

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DR	EMBL; S83543; AAB50734.2; -.
DR	HSSP; P43214; IMHO.
DR	InterPro; IPR000882; Pollen_allergen.
DR	Pfam; PF01357; Pollen_allergen.
DR	PRINTS; PR01225; EXPANSNFAMLY.
DR	ProDom; PD002179; Pollen_allergen; 1.
DR	PROSITE; PS50843; EXPANSIN_CBD; 1.
DR	PROSITE; PS50842; EXPANSIN_EC45; 1.
KW	Allergen.
FT	DOMAIN 39 145 EXPANSIN-LIKE EG45.
FT	DOMAIN 159 240 EXPANSIN-LIKE CBD.
FT	CARBOHYD 9 N-LINKED (GLCNAC...) (POTENTIAL).
SEQUENCE	246 AA; 2688 MW; 43DBD4ZDBA588322 CRR64;

Query Match	20.0%	Score 249.5;	DB 1;	Length 246;
Best Local Similarity	29.28;	Pred. No. 2.4e-15;		
Matches	70;	Conservative 41;	Mismatches 90;	Indels 39.
				Care 0.

```

5 WERHAFFYFG----GADASGTNGAGCGYGNLISQYGIQTALSTALFNSQKCGACBEL 60
   |  ||||  ||  |||||  :|  |||||  |||||  |||||  |||||  |||||  |||||
18 WLEKRAFFYFSNRRGA-APDHHGAGCYADVKRPFDGWTACGNRPFIKDGIGRACAEI 76
   |  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
61 TCDEDFEMCIPGSIIRVYNLALANDNGMCNPLKHFDLAEAFIQTQO-----Y 113
   |  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|
77 KCR-EPEVCSGEVYLKTDKNYE-----HIAAIVHFDLSGACFAGMAKKQGEDKLR 126
   |  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|
114 RAGIVPAVARVRPCEKGGIRFTIN----GNYPDLVLIITWVGACGDIKRAVSLKSGSTQD 169
   |  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|
127 KAGELFLQRRVAVCKPSTKTIPIIEKGSNDHYALLVYKAADGNIIVAVDIKPRDSD 186
   |  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|
170 WQSMNRNMQNNQOSNTY--LRGQSLSFQVTDSDGRTVYVYVPHDY-----QFG 217
   |  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|
187 FIPMKSSGMAIWRIDPKRPLKG-PSISILTSEGGAHILVQDDYIPANMKPDVTYYSKLFQ 245
   |  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|

```

RESULT 6

ID	MP21_MAZE	STANDARD;	PRT;	191 AA.
AC	007154;			
DT	01-FEB-1995	(Rel. 31, Created)		
DT	01-FEB-1995	(Rel. 31, Last sequence update)		
DT	01-MAR-2002	(Rel. 41, Last annotation update)		
DE	Pollen allergen Zea m 1 (Zea m 1).			
DE	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Streptophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida;			
OC	Panicoidae; Andropogoneae; Zea.			
NCBI_TextID=4577;				

RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pollen;
 RX MEDLINE=94010312; PubMed=8406014;
 RA Broadwater A.H., Rubinstein A.L., Chay C.H., Klapper D.G.,
 RT Bedinger P.A.).
 RT "zea m1, the maize homolog of the allergen-encoding lol pi gene of
 RT rye grass.";
 RL Gene 131:227-230(1993).
 CC -! TISSUE SPECIFICITY: POLLEN TISSUE.
 CC -! DEVELOPMENTAL STAGE: EXPRESSION LOW BEFORE AND HIGH AFTER
 CC POLLEN MITOSIS.
 CC -! DISEASE: CAUSES MAIZE POLLEN ALLERGY.
 CC -! SIMILARITY: BELONGS TO THE LOT. P 1 FAMILY OF ALLERGENS.
 CC -! SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EC45 DOMAIN.
 CC -! SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 CC

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EMBL; L14271; AAA33496.1; -.
PIR; JC1524; JC1524.
HSSP; P43214; 1WHO.
MatzEDB; 65840; -.
InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen.
PRINTS; PR01225; EXPANSINFAMILY.
ProDom; PD002179; Pollen_allergen; 1.
ProSITE; PS00843; EXPANSIN_CBD; 1.
ProSITE; PS00842; EXPANSIN_EG45; 1.
W Allergen; Multigene family.
DOMAIN 1 91 EXPANSIN-LIKE EG45.
DOMAIN 105 186 EXPANSIN-LIKE CBD.
SEQUENCE 191 AA; 21362 MW; 6E2A9DF921C45C63 CRC64;

Query Match	17.7%	Score 220;	DB 1;	Length 191;
Best Local Similarity	28.3%;	Pred. No. 7.9e-13;		
Matches	54;	Conservative	39;	Mismatches 70;
				Indels 28.
				Gaps 7.

[illegible]

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CC EMBL: S80654; AAB35984.1; -
DR HSSP: P43214; IMHO.
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen.1.
DR PRINTS: PR01225; EXPANSIN_FAM1.
DR ProDom: PD002179; Pollen_allergen.1.
DR PROSITE: PS00843; EXPANSIN_CBD.1.
DR PROSITE: PS00842; EXPANSIN_EG45.1.
DR Allergen: Glycoprotein; Signal.
KW SIGNAL.
FT CHAIN 1 29 MAJOR POLLEN ALLERGEN PHA A 1.
FT DOMAIN 67 173 EXPANSIN-LIKE EG45.
FT DOMAIN 187 268 EXPANSIN-LIKE CBD.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 37 37 P -> G (IN REF. 2).
SQ SEQUENCE 269 AA; 29011 MW; 058834A58ACE877F CRC64;

Query Match 20.6%; Score 257; DB 1; Length 269;
Best Local Similarity 30.7%; Pred. No. 5.6e-16;
Matches 70; Conservative 35; Mismatches 93; Indels 30; Gaps 9;

OY 5 WERGHATFYGGADASGTM--GGACGYNLHSGYGLQTAALSTALFNSQKCGACFEIITC 62
DB 47 WLDAKSTWYKPGKPGACPKDNGKAGCYKVDKAPFNGMTGCGNTPFKDKRGCGSGCEIIC 106
OY 63 EDDPENCIPGSIIVRYNLNLFALNDNGGMCNPLK--HFDIAEPAFILQIAQ-----Y 113
DB 107 -SKPESCSGEIVYH-----ITDDN---EPIIAPYHFDLSGHAFSGMAKKEEENVR 154
OY 114 RAGIVPAVFRFRPCEKGGGIRFTIN---GNPFDLVLTNNGAGDIRAVLSKSKTDQ 169
DB 155 GAGLELELQFRVVKCKYDDTKRPFHEVKEKSNPVYLAIVKYVDGDDVAVADIKRKGDK 214
OY 170 WQSMRNWQGNQMSNT--YLKGSLSFOVYDSDGRVVSVDVVPDHQD 215
DB 215 WIELKESGAIWRIDTPDKLTG--PTIVRYTTEGGTKAEFEVDVIEGK 261

RESULT 4
MPLI_LOLPR STANDARD; PRT; 263 AA.
AC P14946; P19964;
ID 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Pollen allergen Lol p 1 precursor (Lol p 1) (Allergen R7).
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Poaceae; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-48.
RC TISSUE=pollen;
RX MEDLINE=90375479; PubMed=1697854;
RA Perez M., Ishioka G.Y., Walker L.E., Chesnut R.W.;
RT "CDNA cloning and immunological characterization of the rye grass
RL J. Biol. Chem. 265:16210-16215(1990).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-48.
RC TISSUE=pollen;
RX MEDLINE=91160716; PubMed=2001733;
RA Griffith I.J., Smith P.M., Pollock J., Theerakulpisut P.,
RA Avjoglou A., Davies S., Hough T., Singh M.B., Simpson R.J., Ward L.D.,
RA Knox R.B.;
RT "Cloning and sequencing of Lol pI, the major allergenic protein of
RL rye-grass pollen";
RN FEBS Lett. 279:210-215(1991).
RP SEQUENCE OF 24-53.
RC TISSUE=pollen;
RX MEDLINE=86242068; PubMed=3718469;

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RA Cottam G.P., Moran D.M., Standering R.;
RT "Physicochemical and immunochemical characterization of allergenic
RT proteins from rye-grass (Lolium perenne) pollen prepared by a rapid
RT and efficient purification method.";
RL Biochem. J. 234:305-310(1986).
RN [4]
RP SEQUENCE OF 236-263.
RX MEDLINE=89364850; PubMed=2475768;
RA Esch R.E., Klapper D.G.;
RT "Isolation and characterization of a major cross-reactive grass group
RT I allergenic determinant.";
RL Mol. Immunol. 26:557-561(1989).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P 1 FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
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CC
CC EMBL: M57474; AAA63279.1; -
CC EMBL: M57476; AAA63278.1; -
CC PIR: A23341; A23341.
CC PIR: B37881; B37881.
CC PIR: S13614; S13614.
CC HSSP: P43214; IMHO.
CC InterPro: IPR000882; Pollen_allergen.
CC Pfam: PF01357; Pollen_allergen.1.
CC PRINTS: PR01225; EXPANSIN_FAM1.
CC ProDom: PD002179; Pollen_allergen.1.
CC PROSITE: PS00843; EXPANSIN_CBD.1.
CC PROSITE: PS00842; EXPANSIN_EG45.1.
CC Allergen: Glycoprotein; Signal; Multigene family.
KW SIGNAL.
FT CHAIN 1 23
FT DOMAIN 61 167
FT DOMAIN 181 262
FT CARBOHYD 32 32
FT VARIANT 68 68 N -> D.
FT VARIANT 177 177 A -> G.
FT VARIANT 210 210 I -> T.
FT VARIANT 246 246 F -> V.
FT CONFLICT 28 28 P -> C (IN REF. 3).
FT CONFLICT 31 31 P -> C (IN REF. 3).
FT CONFLICT 48 48 W -> MW (IN REF. 3).
SQ SEQUENCE 263 AA; 28438 MW; 7675896F279C88C9 CRC64;

Query Match 20.4%; Score 254; DB 1; Length 263;
Best Local Similarity 29.8%; Pred. No. 1e-15;
Matches 68; Conservative 37; Mismatches 93; Indels 30; Gaps 9;

OY 5 WERGHATFYGGADASGTM--GGACGYNLHSGYGLQTAALSTALFNSQKCGACFEIITC 62
DB 41 WLDAKSTWYKPGKPGACPKDNGKAGCYKVDKAPFNGMTGCGNTPFKDKRGCGSGCEIIC 100
OY 63 EDDPENCIPGSIIVRYNLNLFALNDNGGMCNPLK--HFDIAEPAFILQIAQ-----Y 113
DB 101 -TPKESCSGEIVYH-----ITDDN---EPIIAPYHFDLSGHAFSGMAKKEEENVR 148
OY 114 RAGIVPAVFRFRPCEKGGGIRFTIN---GNPFDLVLTNNGAGDIRAVLSKSKTDQ 169
DB 149 GAGLELELQFRVVKCKYDDTKRPFHEVKEKSNPVYLAIVKYVDGDDVAVADIKRKGDK 208
OY 170 WQSMRNWQGNQMSNT--YLKGSLSFOVYDSDGRVVSVDVVPDHQD 215
DB 209 WIELKESGAIWRIDTPDKLTG--PTIVRYTTEGGTKAEFEVDVIEGK 255

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OY 5 WERGHATFYGGADASCTM--GCACGYGNLHSGYGLDTALSTALFNSGKGCACFELTC 62
DB 41 WLDKSTWYKPRPGACPRKNGCAGCKVDKPPSGMTGCGGNTPIKSGGSCSEFELIC 100
OY 63 EDDPENCIPGSIIVRYNLANFALANDNGWCNPLK--HFDLAEPFLQIAQ-----Y 113
DB 101 -TRFECSCGEPYVH-----ITDDN-----EPIAPYHFDLSGHAFGAMAKKGEQKLR 148
OY 114 RAGIVPAFRFRPCCEKGGIRFTIN---GNPYFDLVLTNNVGAGDIRAVSLKSKSTQ 169
DB 149 SAGLELQFRVRCCKYKPEFHEKGSNPYLLALVYIDGDDVAVADIKKCKDK 208
OY 170 WQSMRNMGQNMOSNT--YLRGSLSFQVYTDSDGRTVVSVDVPHDMPGCFTE 221
DB 209 WIELKESWGAIVMDTPDKLTG--PFTVRYTTGCTGTEADVIPECKADTSTE 261

RESULT 2
MPAL_HOLLA STANDARD: PRT; 265 AA.
AC P43216: Q39975;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Major pollen allergen Hol 1 precursor (Hol 1 I) (Hol 1 I.0101 and
DE 1.0102).
OS Holcus lanatus (Velvet grass).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: Lillipsida: Poales: Poaceae: Poideae:
OC Poaceae: Holcus.
OX NCBI_TaxID=29679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. AVENAE; TISSUE=Pollen;
RA Schramm G.D., Bufe A., Becker W.M., Schlaak M.;
RT Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 18-265 FROM N.A.
RC STRAIN=CV. AVENAE; TISSUE=Pollen;
RA MEDLINE=97358126; PubMed=9215246;
RA Schramm G.D., Bufe A., Petersen A., Haas H., Schlaak M., Becker W.M.;
RT "Mapping of IgE-binding epitopes on the recombinant major group I
RT allergen of velvet grass pollen, rHol 1 I.";
RL J. Allergy Clin. Immunol. 99:781-787(1997).
RN [3]
RP CHARACTERIZATION.
RP STRAIN=CV. AVENAE; TISSUE=Pollen;
RC MEDLINE=96319506; PubMed=8768803;
RA Schramm G.D., Petersen A., Bufe A., Schlaak M., Becker W.M.;
RT "Identification and characterization of the major allergens of velvet
RT grass (Holcus lanatus), Hol 1 I and Hol 1.5.";
RL Int. Arch. Allergy Immunol. 110:354-363(1996).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
CC -----
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CC -----
DR EMBL: Z27084; CAA81610.1;
DR EMBL: Z68893; CAA93121.1;
DR HSSP: P43214; 1WHO.
DR InterPro: IPR000882; Pollen.allergen.
DR Pfam: PF01357; Pollen.allergen.1.
DR PRINTS: PR01225; EXPANSINFAMLY.
DR ProDom: PD002179; Pollen.allergen.1.

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DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen; Signal.
FT SIGNAL 1 25
FT CHAIN 26 265
FT DOMAIN 63 169 MAJOR POLLEN ALLERGEN HOL 1.1.
FT DOMAIN 183 264 EXPANSIN-LIKE EG45.
FT VARIANT 103 103 EXPANSIN-LIKE CBD.
FT VARIANT 103 103 T -> S (IN HOL 1.1.0102).
SQ SEQUENCE 265 AA; 28590 MW; 1FE23B3FE198AD6D CRC64;

Query Match 20.6%; Score 257; DB 1; Length 265;
Best Local Similarity 29.1%; Pred. No. 5.5e-16;
Matches 68; Conservative 40; Mismatches 96; Indels 30; Gaps 9;

OY 5 WERGHATFYGGADASCTM--GCACGYGNLHSGYGLDTALSTALFNSGKGCACFELTC 62
DB 43 WLDKSTWYKPRPGACPRKNGCAGCKVDKPPSGMTGCGGNTPIFKOSRGSCSEFELIC 102
OY 63 EDDPENCIPGSIIVRYNLANFALANDNGWCNPLK--HFDLAEPFLQIAQ-----Y 113
DB 103 -TRFECSCGEPYVH-----ITDDN-----EPIAPYHFDLSGHAFGAMAKKGEQKLR 150
OY 114 RAGIVPAFRFRPCCEKGGIRFTIN---GNPYFDLVLTNNVGAGDIRAVSLKSKSTQ 169
DB 151 SAGLELQFRVRCCKYKPEFHEKGSNPYLLALVYIDGDDVAVADIKKCKDK 210
OY 170 WQSMRNMGQNMOSNT--YLRGSLSFQVYTDSDGRTVVSVDVPHDMPGCFTE 221
DB 211 WIELKESWGAIVMDTPDKLTG--PFTVRYTTGCTGTEADVIPECKADTSTE 263

RESULT 3
MPAL_PHAQO STANDARD: PRT; 269 AA.
AC Q41260;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Major pollen allergen Pha a 1 precursor (Pha a I).
DE Phalaris aquatica (Canary grass).
OS Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: Lillipsida: Poales: Poaceae: Poideae:
OC Poaceae: Phalaris.
OX NCBI_TaxID=28479;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RA MEDLINE=96105569; PubMed=8564724;
RA Supphloglu C., Singh M.B.;
RT Cloning, sequencing and expression in Escherichia coli of Pha a 1
RT and four isoforms of Pha a 5, the major allergens of canary grass
RT pollen.";
RL Clin. Exp. Allergy 25:853-865(1995).
RN [2]
RP SEQUENCE OF 30-49.
RC MEDLINE=93319091; PubMed=7687099;
RA Supphloglu C., Singh M.B., Simpson R.J., Ward L., Knox R.B.;
RT "Identification of canary grass (Phalaris aquatica) pollen allergens
RT by immunoblotting: IgE and IgG antibody-binding studies.";
RL Allergy 48:273-281(1993).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
CC -----
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:50:30 : Search time 5.8181 Seconds
(without alignments)
1499.000 Million cell updates/sec

Title: US-09-896-301-5

Sequence: 1 DNGWGRGHAFYFGADASG.....SYDVVPHDMQFGTFEGGQF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	272	21.8	263	1	MPPL_PHLPR
2	257	20.6	265	1	MPPL_HOLLA
3	257	20.6	265	1	MPPL_PHLPR
4	254	20.4	263	1	MPPL_PHLPR
5	249.5	20.0	246	1	MPPL_PHLPR
6	220	17.7	191	1	MPPL_PHLPR
7	216.5	17.4	263	1	MPPL_PHLPR
8	99	8.0	242	1	MPPL_PHLPR
9	97.5	7.8	333	1	MPPL_PHLPR
10	89	7.1	461	1	MPPL_PHLPR
11	87.5	7.0	181	1	MPPL_PHLPR
12	85.5	6.9	97	1	MPPL_PHLPR
13	85.5	6.9	1250	1	MPPL_PHLPR
14	83	6.7	463	1	MPPL_PHLPR
15	81	6.5	418	1	MPPL_PHLPR
16	81	6.5	878	1	MPPL_PHLPR
17	80.5	6.5	1744	1	MPPL_PHLPR
18	79.5	6.4	1974	1	MPPL_PHLPR
19	79	6.3	564	1	MPPL_PHLPR
20	79	6.3	870	1	MPPL_PHLPR
21	79	6.3	1192	1	MPPL_PHLPR
22	78.5	6.3	373	1	MPPL_PHLPR
23	78	6.3	1545	1	MPPL_PHLPR
24	77.5	6.2	316	1	MPPL_PHLPR
25	77.5	6.2	326	1	MPPL_PHLPR
26	77.5	6.2	1592	1	MPPL_PHLPR
27	77	6.2	386	1	MPPL_PHLPR
28	77	6.2	462	1	MPPL_PHLPR
29	77	6.2	2334	1	MPPL_PHLPR
30	76.5	6.1	771	1	MPPL_PHLPR
31	76	6.1	466	1	MPPL_PHLPR
32	76	6.1	1172	1	MPPL_PHLPR
33	75.5	6.1	378	1	MPPL_PHLPR

34	75	6.0	254	1	YVON_BACSU
35	75	6.0	486	1	GIGA_THENA
36	74.5	6.0	173	1	FLAV_HAELN
37	74.5	6.0	570	1	STIM_DROME
38	74.5	6.0	755	1	TRZM_AGR4
39	74.5	6.0	798	1	HMBP_DROME
40	74.5	6.0	1541	1	ICAI_HAELN
41	74	5.9	482	1	SYP_METTH
42	74	5.9	1222	1	PWSP_HUMAN
43	74	5.9	2327	1	CCAB_MOUSE
44	74	5.9	2336	1	CCAB_RAT
45	74	5.9	2339	1	CCAB_HUMAN

ALIGNMENTS

RESULT 1
MPPL_PHLPR STANDARD: PRT: 263 AA.
AC P43213;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Pollen allergen Phl p 1 precursor (Phl p 1).
GN PHLP1.
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RX MEDLINE=95015525; PubMed=7930302;
RA Laifer S., Valencia R., Vrtala S., Susani M., van Ree R., Kraft D.,
RT Scheiner O., Duchene M.;
RT "Complementary DNA cloning of the major allergen Phl p 1 from timothy
RT grass (Phleum pratense); recombinant Phl p 1 inhibits IgE binding to
RT group I allergens from eight different grass species.";
RL J. Allergy Clin. Immunol. 94:689-698(1994).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE LOI p 1 FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
CC
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CC -----
CC EMBL: X78813; CA55390.1; -.
CC HSSP: P43214; IMHO.
DR InterPro: IPR000882; Pollen allergen.
DR Pfam: PF01357; Pollen allergen; 1.
DR PRINTS: PR01225; EXPANSIN_FAM1.
DR PROSITE: PS002179; Pollen allergen; 1.
DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 23
FT CHAIN 1 263
FT DOMAIN 24 61
FT DOMAIN 61 167
FT DOMAIN 181 262
FT CARBOHYD 32 32
SQ SEQUENCE 263 AA; 28457 MW; 046BA249C17BC048 CRC64;
Query Match 21.88; Score 272; DB 1; Length 263;
Best Local Similarity 29.9%; Pred. No. 2.5e-17;
Matches 70; Conservative 41; Mismatches 93; Indels 30; Gaps 9;

01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE EXPANSIN (FRAGMENT).
 OC Pinus taeda (loblolly pine).
 OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 NCBI_TaxID=3352;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=HYPOCOTYL;
 RA Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
 RT "Expansins are conserved in conifers and expressed in response to
 exogenous auxin."
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64891; AAB40635.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMLY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 FT NON_TER 1
 SO SEQUENCE 232 AA; 24745 MW; 134080573DE907CF CRC64;

Query Match 74.5%; Score 927; DB 10; Length 232;
 Best Local Similarity 72.9%; Pred. No. 1.le-78;
 Matches 164; Conservative 26; Mismatches 31; Indels 4; Gaps 2;

OY 3 GGMERGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGCKGACFELTC 62
 DB 8 GGMESAHATFYGGSDAGTGMGACGYGNLHSGYGLQTAALSTALFNDGLSCGACTEMRC 67
 OY 63 EDDPENCIPGSIIV--RYNLANFALANDGWCNPLKHFDLAEPALQIAQYRAGIVP 119
 DB 68 NDDPQWCLPGRVYVATNFCPPNNALRPNDGWCNPLQHFDMAPFLAKYRGIVP 127
 OY 120 VAFRRVPCCKGIRFTTNGNPNFYDLVLTINVGAGADIRAVSLKSKTDQMSRMWQ 179
 DB 128 ILTYRVCLRKGGIRFTVNGHSHYFNLVLTINVGAGADVAHVSIGSRSG-WQPMSSRMWQ 186
 OY 180 NMOSNTYLRGOSLSFOVTDSDGRTVVSVDVYPHDMQFGOTFEQGO 224
 DB 187 NMOSNTYLRGOSLSFOVTDSDGRTVVSNNVAPSNMFGOTFEQGO 231
 RESULT 14
 P93495 PRELIMINARY; PRT; 232 AA.
 ID P93495.
 AC P93495.
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE EXPANSIN (FRAGMENT).
 OC Pinus taeda (loblolly pine).
 OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 NCBI_TaxID=3352;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=HYPOCOTYL;
 RA Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
 RT "Expansins are conserved in conifers and expressed in response to
 exogenous auxin."
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64893; AAB40637.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMLY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 FT NON_TER 1
 SO SEQUENCE 232 AA; 24694 MW; 9238EACD9E1FEC5E CRC64;

Query Match 74.5%; Score 927; DB 10; Length 232;
 Best Local Similarity 72.9%; Pred. No. 1.le-78;
 Matches 164; Conservative 26; Mismatches 31; Indels 4; Gaps 2;

OY 3 GGMERGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGCKGACFELTC 62
 DB 8 GGMESAHATFYGGSDAGTGMGACGYGNLHSGYGLQTAALSTALFNDGLSCGACTEMRC 67
 OY 63 EDDPENCIPGSIIV--RYNLANFALANDGWCNPLKHFDLAEPALQIAQYRAGIVP 119
 DB 68 NDDPQWCLPGRVYVATNFCPPNNALRPNDGWCNPLQHFDMAPFLAKYRGIVP 127
 OY 120 VAFRRVPCCKGIRFTTNGNPNFYDLVLTINVGAGADIRAVSLKSKTDQMSRMWQ 179
 DB 128 ILTYRVCLRKGGIRFTVNGHSHYFNLVLTINVGAGADVAHVSIGSRSG-WQPMSSRMWQ 186
 OY 180 NMOSNTYLRGOSLSFOVTDSDGRTVVSVDVYPHDMQFGOTFEQGO 224
 DB 187 NMOSNTYLRGOSLSFOVTDSDGRTVVSNNVAPSNMFGOTFEQGO 231

RESULT 15
 O9SWY1 PRELIMINARY; PRT; 253 AA.
 ID O9SWY1.
 AC O9SWY1.
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE EXPANSIN.
 OC Pinus taeda (loblolly pine).
 OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 NCBI_TaxID=3352;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=HYPOCOTYL;
 RA Hutchison K.W., Singer P.B., McIntosh S., Diaz-Sala C., Greenwood M.S.;
 RT "Expansins are conserved in conifers and expressed in hypocotyls in
 response to exogenous auxin."
 RL Plant Physiol. 120:827-832(1999).
 DR EMBL: AF085330; AAD47901.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMLY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 SO SEQUENCE 253 AA; 27150 MW; 2675BB1569BD75D4 CRC64;

Query Match 74.5%; Score 927; DB 10; Length 253;
 Best Local Similarity 72.9%; Pred. No. 1.le-78;
 Matches 164; Conservative 26; Mismatches 31; Indels 4; Gaps 2;

OY 3 GGMERGHATFYGGADAGTGMGACGYGNLHSGYGLQTAALSTALFNSGCKGACFELTC 62
 DB 29 GGMESAHATFYGGSDAGTGMGACGYGNLHSGYGLQTAALSTALFNDGLSCGACTEMRC 88
 OY 63 EDDPENCIPGSIIV--RYNLANFALANDGWCNPLKHFDLAEPALQIAQYRAGIVP 119
 DB 89 NDDPQWCLPGRVYVATNFCPPNNALRPNDGWCNPLQHFDMAPFLAKYRGIVP 148
 OY 120 VAFRRVPCCKGIRFTTNGNPNFYDLVLTINVGAGADIRAVSLKSKTDQMSRMWQ 179
 DB 149 ILTYRVCLRKGGIRFTVNGHSHYFNLVLTINVGAGADVAHVSIGSRSG-WQPMSSRMWQ 207
 OY 180 NMOSNTYLRGOSLSFOVTDSDGRTVVSVDVYPHDMQFGOTFEQGO 224
 DB 208 NMOSNTYLRGOSLSFOVTDSDGRTVVSNNVAPSNMFGOTFEQGO 252

Search completed: October 11, 2002, 14:59:41
 Job time : 19.428 secs

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE EXPANSIN.
 GN EXP2.
 OS Prunus armeniaca (Apricot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxId=36596;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERGERON; TISSUE=MESOCARP, EXOCARP.
 RA Mdeguite-A-Mdeguite D., Fils-Lycaon B.;
 RT "Molecular cloning and nucleotide sequence of expansin 2 (Pa-Exp2)
 RT from apricot fruit."
 RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF038815; AAC33530.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNPFAMLY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 SO SEQUENCE 252 AA; 26758 MW; 5B81AE5C8E959791 CRC64;

Query Match 76.7%; Score 954.5; DB 10; Length 252;
 Best Local Similarity 76.5%; Pred. No. 3.4e-81;
 Matches 173; Conservative 21; Mismatches 27; Indels 5; Gaps 3;

QY 3 GGEHGATFTYGGADASGTMGACGYGNLSOGYGLQTAALSTALFNSGQKGCAGFELTC 62
 DB 29 GGEHGATFTYGGADASGTMGACGYGNLSOGYGLQTAALSTALFNSGQKGCAGFELTC 88
 QY 63 EDDPENCIPGSIIV--RYNLANFALANDNGWCNPPLEKHFDLAPFLQIAOYRAGIIV 119
 DB 89 DSDPKWCLEPGSIIVATNCPNLAQSNNDNGWCNPPLEKHFDLAPFLQIAOYRAGIIV 148
 QY 120 VAFRRVPCCKGGGIRFTTNGNPFYDLVLTNNAGADIRAVSLKSKTDQMSRMNGQ 179
 DB 149 ISRRVSCVKKGGIRFTTNGNPFYDLVLTNNAGADIRAVSLKSKTDQMSRMNGQ 207
 QY 180 NMOSNTYLRGQSLSPQVTDSDGRVTSYDVYPHDMQFGQTEGGQF 225
 DB 208 NMOSNTYLRGQSLSPQVTDSDGRVTSYDVYPHDMQFGQTEGGQF 252

RESULT 11
 Q9FS30 PRELIMINARY; PRT; 252 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE EXPANSIN.
 GN PPEXPI.
 OS Prunus persica (Peach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxId=3760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hayama H.;
 RT "Homolog to expansin in peach fruit."
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB029083; BAB19676.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PR01225; EXPANSNPFAMLY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 SO SEQUENCE 252 AA; 26743 MW; BF0B86FE0C060482 CRC64;

Query Match 76.3%; Score 950.5; DB 10; Length 252;
 Best Local Similarity 76.5%; Pred. No. 8.1e-81;
 Matches 173; Conservative 21; Mismatches 27; Indels 5; Gaps 3;

QY 3 GGEHGATFTYGGADASGTMGACGYGNLSOGYGLQTAALSTALFNSGQKGCAGFELTC 62

DB 29 GGEHGATFTYGGADASGTMGACGYGNLSOGYGLQTAALSTALFNSGQKGCAGFELTC 88
 QY 63 EDDPENCIPGSIIV--RYNLANFALANDNGWCNPPLEKHFDLAPFLQIAOYRAGIIV 119
 DB 89 DSDPKWCLEPGSIIVATNCPNLAQSNNDNGWCNPPLEKHFDLAPFLQIAOYRAGIIV 148
 QY 120 VAFRRVPCCKGGGIRFTTNGNPFYDLVLTNNAGADIRAVSLKSKTDQMSRMNGQ 179
 DB 149 ISRRVSCVKKGGIRFTTNGNPFYDLVLTNNAGADIRAVSLKSKTDQMSRMNGQ 207
 QY 180 NMOSNTYLRGQSLSPQVTDSDGRVTSYDVYPHDMQFGQTEGGQF 225
 DB 208 NMOSNTYLRGQSLSPQVTDSDGRVTSYDVYPHDMQFGQTEGGQF 252

RESULT 12
 Q9SRT1 PRELIMINARY; PRT; 253 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE EXPANSIN.
 GN EXP2.
 OS Fragaria ananassa (Strawberry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
 OX NCBI_TaxId=3747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV CHANDLER.
 RA Civeello P.M., Sabehat A., Powell A.L.T., Bennett A.B.;
 RT "An expansin gene expressed in ripening strawberry fruit is auxin-
 RT independent."
 RL Plant Physiol. 12:1273-1279(1999).
 DR EMBL: AF159563; AAF21101.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNPFAMLY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 DR Prosite: PS00626; RC1.2; UNKNOWN.1.
 SO SEQUENCE 253 AA; 26887 MW; CB39CF00ADAE1CEF CRC64;

Query Match 75.8%; Score 944; DB 10; Length 253;
 Best Local Similarity 76.4%; Pred. No. 3.3e-80;
 Matches 172; Conservative 18; Mismatches 31; Indels 4; Gaps 2;

QY 4 GGEHGATFTYGGADASGTMGACGYGNLSOGYGLQTAALSTALFNSGQKGCAGFELTC 63
 DB 30 GGEHGATFTYGGADASGTMGACGYGNLSOGYGLQTAALSTALFNSGQKGCAGFELTC 89
 QY 64 DDPENCIPGSIIV--RYNLANFALANDNGWCNPPLEKHFDLAPFLQIAOYRAGIIV 120
 DB 90 DDPENCIPGSIIVATNCPNLAQSNNDNGWCNPPLEKHFDLAPFLQIAOYRAGIIV 149
 QY 121 AFRVPCCKGGGIRFTTNGNPFYDLVLTNNAGADIRAVSLKSKTDQMSRMNGQ 180
 DB 150 SFRVPCCKGGGIRFTTNGNPFYDLVLTNNAGADIRAVSLKSKTDQMSRMNGQ 208
 QY 181 WOSTYLRGQSLSPQVTDSDGRVTSYDVYPHDMQFGQTEGGQF 225
 DB 209 WOSTYLRGQSLSPQVTDSDGRVTSYDVYPHDMQFGQTEGGQF 253

RESULT 13
 P93493 PRELIMINARY; PRT; 232 AA.

DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)

RT extension in plants.
 Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
 DR EMBL: U30382; AAB37746.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen.1.
 DR PRINTS: PD01225; EXPANSFAMLY.
 DR ProDom: PD002179; Pollen_allergen.1.
 RT CHAIN 24 250 EXPANSIN SL.
 SO SEQUENCE 250 AA; 27215 MW; 60651BC47EA186DA CRC64;

Query Match 77.3%; Score 962; DB 10; Length 250;
 Best Local Similarity 74.3%; Pred. No. 6, 8e-82;
 Matches 171; Conservative 26; Mismatches 27; Indels 4; Gaps 2;

QY 1 DNGGEMGHATFYGGADASTMGACGCGYGNLHSGYGLQTAALSTALFNSGCGACFEL 60
 DB 24 DYGGMOSHATFYGGADASTMGACGCGYGNLHSGYGLQTAALSTALFNSGCGACFEL 83
 QY 61 TCEDDPEMCIPGSIIV--RYNLAFALANDGNCNPLKHFDAEPALQIAOYRA 117
 DB 84 TCTNDPRKMCIPGSIIV--RYNLAFALANDGNCNPLKHFDAEPALQIAOYRA 143
 QY 118 VPAFAFRVPCCKGIRFTINGNPFYDLVLTNNGACDIAVSLKSKTDQMSMR 177
 DB 144 VPAFAFRVPCCKGIRFTINGNPFYDLVLTNNGACDIAVSLKSKTDQMSMR 202
 QY 178 GOMGMSNTYLRGQSLSFQVTDSDGRTVSYDVPHDMQFGTFEGGQF 225
 DB 203 GOMGMSNTYLRGQSLSFQVTDSDGRTVSYDVPHDMQFGTFEGGQF 250

RESULT 8
 022874 PRELIMINARY; PRT: 253 AA.

AC 022874
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE EXPANSIN.
 GN ATG240610.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_Taxid=3702;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Gaitera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana."
 RT thaliana."
 RL Nature 402:761-768(1999).
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX LIn X.;
 RL EMBL: AC002336; AAB87577.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen.1.
 DR PRINTS: PD01225; EXPANSFAMLY.
 DR ProDom: PD002179; Pollen_allergen.1.
 SO SEQUENCE 253 AA; 27260 MW; 08C42860D523DD8A CRC64;

Query Match 77.0%; Score 958.5; DB 10; Length 253;
 Best Local Similarity 74.3%; Pred. No. 1, 5e-81;

Matches 171; Conservative 23; Mismatches 29; Indels 7; Gaps 2;

QY 1 DNGGEMGHATFYGGADASTMGACGCGYGNLHSGYGLQTAALSTALFNSGCGACFEL 60
 DB 26 DYGGMOSHATFYGGADASTMGACGCGYGNLHSGYGLQTAALSTALFNSGCGACFEL 85
 QY 61 TCEDDPEMCIPGSIIVRYNLAF-----ALANDGNCNPLKHFDAEPALQIAOYRA 115
 DB 86 KCNDPRKMCIPGSIIV--TATNFCPPNPGLSNDGNCNPLKHFDAEPALQIAOYRA 143
 QY 116 GIVPAFAFRVPCCKGIRFTINGNPFYDLVLTNNGACDIAVSLKSKTDQMSMR 175
 DB 144 GIVPAFAFRVPCCKGIRFTINGNPFYDLVLTNNGACDIAVSLKSKTDQMSMR 203
 QY 176 MWGOMGMSNTYLRGQSLSFQVTDSDGRTVSYDVPHDMQFGTFEGGQF 225
 DB 204 MWGOMGMSNTYLRGQSLSFQVTDSDGRTVSYDVPHDMQFGTFEGGQF 253

RESULT 9

09FNT0 PRELIMINARY; PRT: 260 AA.

AC 09FNT0
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE EXPANSIN.
 OS Cicer arietinum (chickpea) (Garbanzo).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
 OX NCBI_Taxid=3827;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
 RX Duplico B., Sanchez M.A., Labrador E.;
 RT "An second expansin is expressed in chickpea epicotyls."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ291817; CAC19184.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR ProDom: PD000504; RRM.
 DR PRINTS: PD01225; EXPANSFAMLY.
 DR ProDom: PD002179; Pollen_allergen.1.
 DR ProSite: PS00030; RRM_RNP_1; UNKNOWN.1.
 SO SEQUENCE 260 AA; 28266 MW; 32A70368ED288395 CRC64;

Query Match 76.9%; Score 957; DB 10; Length 260;
 Matches 172; Conservative 23; Mismatches 27; Indels 8; Gaps 3;

QY 1 DNGGEMGHATFYGGADASTMGACGCGYGNLHSGYGLQTAALSTALFNSGCGACFEL 60
 DB 34 DYGGMOSHATFYGGADASTMGACGCGYGNLHSGYGLQTAALSTALFNSGCGACFEL 93
 QY 61 TCEDDPEMCIPGSIIVRYNLAF-----ALANDGNCNPLKHFDAEPALQIAOYRA 115
 DB 94 KCNDPRKMCIPGSIIV--TATNFCPPNPGLSNDGNCNPLKHFDAEPALQIAOYRA 151
 QY 116 GIVPAFAFRVPCCKGIRFTINGNPFYDLVLTNNGACDIAVSLKSKTDQMSMR 175
 DB 152 GIVPAFAFRVPCCKGIRFTINGNPFYDLVLTNNGACDIAVSLKSKTDQMSMR 210
 QY 176 MWGOMGMSNTYLRGQSLSFQVTDSDGRTVSYDVPHDMQFGTFEGGQF 225
 DB 211 MWGOMGMSNTYLRGQSLSFQVTDSDGRTVSYDVPHDMQFGTFEGGQF 260

RESULT 10

081133 PRELIMINARY; PRT: 252 AA.

AC 081133
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

QY 1 DNGMGRHATFEYGGADASCTMGACGYNLHSGYGLQTAALSTALFNSGKCGACFEL 60
 DB 28 DNGMGRHATFEYGGADASCTMGACGYNLHSGYGLQTAALSTALFNSGKCGACFEL 87
 OY 61 TCEDDEPENCIPGSIIV---RYNLANFALANDNGMCNPPKHPDLAEPALQIAOYRAGI 117
 DB 88 TCEDDEPENCIPGSIIVSATNFCPPNFALANDNGMCNPPKHPDLAEPALQIAOYRAGI 147
 OY 118 VPAFAFRVPCPEKGGIRFTINGNPFYDLVLTINVGAGDIRAVSLKSGSKTDQMSRNM 177
 DB 148 VPAFAFRVPCPEKGGIRFTINGNPFYDLVLTINVGAGDIRAVSLKSGSKTDQMSRNM 207
 OY 178 GQNMOSNTYLKRGOSLSFOVYTDSDGRTVVSVDVPHDMQFGQTFEGGQF 225
 DB 208 GQNMOSNTYLKRGOSLSFOVYTDSDGRTVVSVDVPHDMQFGQTFEGGQF 255

RESULT 2

O9FLC5 PRELIMINARY: PRT: 255 AA.
 AC O9FLC5: 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE EXPANSIN AF-EXP2
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 ON NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=96344145; PubMed=9679202;
 RA Tanaka T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
 RT features of the regions of 1,381,565 bp covered by twenty one
 RT physically assigned P1 and TMC clones."
 RL DNA Res. 5:131-143(1996).
 DR EMBL: AB010692; BAR09972.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 SO SEQUENCE 255 AA; 27749 MW; 53E678633B2C4152 CRC64;

Query Match 96.2%; Score 1197.5; DB 10; Length 255;
 Best Local Similarity 96.1%; Pred. No. 7.4e-104;
 Matches 219; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

OY 1 DNGMGRHATFEYGGADASCTMGACGYNLHSGYGLQTAALSTALFNSGKCGACFEL 60
 DB 28 DNGMGRHATFEYGGADASCTMGACGYNLHSGYGLQTAALSTALFNSGKCGACFEL 87
 OY 61 TCEDDEPENCIPGSIIV---RYNLANFALANDNGMCNPPKHPDLAEPALQIAOYRAGI 117
 DB 88 TCEDDEPENCIPGSIIVSATNFCPPNFALANDNGMCNPPKHPDLAEPALQIAOYRAGI 147
 OY 118 VPAFAFRVPCPEKGGIRFTINGNPFYDLVLTINVGAGDIRAVSLKSGSKTDQMSRNM 177
 DB 148 VPAFAFRVPCPEKGGIRFTINGNPFYDLVLTINVGAGDIRAVSLKSGSKTDQMSRNM 207
 OY 178 GQNMOSNTYLKRGOSLSFOVYTDSDGRTVVSVDVPHDMQFGQTFEGGQF 225
 DB 208 GQNMOSNTYLKRGOSLSFOVYTDSDGRTVVSVDVPHDMQFGQTFEGGQF 255

RESULT 3

O9LNB2 PRELIMINARY: PRT: 245 AA.
 AC O9LNB2: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE EXPANSIN 2.
 OS Zinnia elegans.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
 OC Helianthaceae; Zinnia.
 ON NCBI_TaxID=34245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20317189; PubMed=10859177;
 RA Im K.H., Cosgrove D.J., Jones A.M.;
 RT "Subcellular localization of expansin mRNA in xylem cells."
 RL Plant Physiol. 123:463-470(2000).
 DR EMBL: AF230332; AAF35901.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 SO SEQUENCE 245 AA; 26201 MW; F6E26114C27E360 CRC64;

Query Match 78.9%; Score 982; DB 10; Length 245;
 Best Local Similarity 75.9%; Pred. No. 9e-84;
 Matches 173; Conservative 25; Mismatches 22; Indels 8; Gaps 3;

OY 3 GQMGHATFEYGGADASCTMGACGYNLHSGYGLQTAALSTALFNSGKCGACFEL 62
 DB 21 GQMGHATFEYGGADASCTMGACGYNLHSGYGLQTAALSTALFNSGKCGACFEL 80
 OY 63 EDDPENCIPGSIIVRYNLANF-----ALANDNGMCNPPKHPDLAEPALQIAOYRAGI 117
 DB 81 NDDPKMCLPGSIIV--TATNFCPPNFGSLNDNGMCNPPKHPDLAEPALQIAOYRAGI 138
 OY 118 VPAFAFRVPCPEKGGIRFTINGNPFYDLVLTINVGAGDIRAVSLKSGSKTDQMSRNM 177
 DB 139 VPISTFORVPCVKGGVFTINGHSYENFLITINVGAGDIRAVSLKSGSKTDQMSRNM 197
 OY 178 GQNMOSNTYLKRGOSLSFOVYTDSDGRTVVSVDVPHDMQFGQTFEGGQF 225
 DB 198 GQNMOSNTYLKRGOSLSFOVYTDSDGRTVVSVDVPHDMQFGQTFEGGQF 245

RESULT 4

O9FUM3 PRELIMINARY: PRT: 254 AA.
 AC O9FUM3: 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE EXPANSIN 1.
 OS Prunus avium (Cherry), and
 OS Prunus cerasus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC eustosids II; Rosales; Rosaceae; Amygdaloideae; Prunus.
 ON NCBI_TaxID=42229, 140311;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P. avium;
 RA Wu Z., Wiersma P.A.;
 RT "Differential Expression of Expansin Genes Isolated from Sweet Cherry
 RT (Prunus avium L.) during Fruit Ripening."
 RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P. cerasus; TISSUE=RIPE FRUIT;
 RA Yoo S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.;
 RT "Coordinated expression of genes encoding expansins and other cell
 RT wall-modifying enzymes is associated with pectin-related changes in
 RT the cell wall during ripening of cherry (P. cerasus) fruit."
 RL Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:51:00 ; Search time 19.428 seconds
(without alignments)
2003.488 Million cell updates/sec

Title: US-09-896-301-5
Perfect score: 1245
Sequence: 1 DNGMGHGHATFGGADASG.....SYDVPHDMQFGQTGGGQF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_19:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.rodent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*
- 15: sp.rvivirus:*
- 16: sp.bacteriophage:*
- 17: sp.archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1203.5	96.7	255	10	Q38866
2	1197.5	96.2	255	10	Q9FLC5
3	982	78.9	245	10	Q9LFB2
4	972	78.1	254	10	Q9FLM3
5	970	77.9	254	10	Q82093
6	963	77.3	253	10	Q93XP2
7	962	77.3	250	10	Q93625
8	958.5	76.9	253	10	Q22874
9	957	76.7	250	10	Q9FNT0
10	954.5	76.3	252	10	Q81133
11	950.5	75.8	252	10	Q9FS30
12	944	75.8	253	10	Q9SRT1
13	927	74.5	232	10	P93493
14	927	74.5	232	10	P93495
15	927	74.5	253	10	Q9SWY1
16	923	74.1	232	10	P93492

17	919.5	73.9	253	10	Q9SMD4
18	912	73.3	232	10	P93494
19	912	73.3	249	10	Q9LDR9
20	912	73.3	258	10	Q49194
21	905	72.7	247	10	Q82625
22	901	72.4	249	10	Q92P35
23	898	72.1	251	10	Q946J1
24	886	71.2	247	10	Q9M517
25	884	71.0	246	10	P93442
26	883.5	71.0	242	10	Q9LBI1
27	883	70.9	246	10	Q946J0
28	883	70.9	251	10	Q40636
29	876	70.4	249	10	Q93XP1
30	875	70.3	252	10	Q94FT7
31	871	70.0	253	10	Q93625
32	869	69.8	237	10	Q93625
33	869	69.8	250	10	Q9C554
34	868	69.7	248	10	Q80622
35	866.5	69.6	249	10	Q9M515
36	858	68.9	255	10	Q9FMA0
37	851	68.4	249	10	Q92P36
38	851	68.4	257	10	Q48818
39	850	68.3	262	10	Q80932
40	849	68.2	239	10	Q92P31
41	846	68.0	250	10	Q9FVG9
42	846	68.0	260	10	Q9M2S9
43	844	67.8	258	10	Q41043
44	840	67.5	260	10	Q93XP0
45	834	67.0	257	10	Q9XG16

ALIGNMENTS

RESULT 1

ID Q38866 PRELIMINARY: PRT: 255 AA.

AC Q38866;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE EXPANSIN AT-EXP2.

GN AT-EXP2.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Kosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=96016146; PubMed=7568110;

RX Sheherban T.Y., Shi J., Durachko D.M., Gulltinan M.J.,

RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;

RT "Molecular cloning and sequence analysis of expansins--a highly

RT conserved, multigene family of proteins that mediate cell wall

RT extension in plants.";

RT Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).

RL [2]

RP SEQUENCE FROM N.A.

RA Sheherban T.Y., Shi J., Durachko D.M., Gulltinan M.J.,

RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;

RA Submitted (MAR-2001) to the EMBL/GenBank/DBD databases.

DR EMBL: U30481; AAB38073.1; -

DR InterPro: IPR000882; Pollen.allergen.

DR Pfam: PF01357; Pollen.allergen; 1.

DR PRINTS: PD001225; EXPANSINFAMLY.

DR ProDom: PD002179; Pollen.allergen; 1.

SQ SQUIDENCE 235 AA; 27B5F0827A285500 CRC64;

Query Match 96.7%; Score 1203.5; DB 10; Length 255;

Best Local Similarity 96.5%; Pred. No. 2e-104;

Matches 220; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

PR 14-MAY-1999: 99US-0134370.
PR 18-MAY-1999: 99US-0134768.
PR 19-MAY-1999: 99US-0134941.
PR 20-MAY-1999: 99US-0135124.
PR 21-MAY-1999: 99US-0135353.
PR 24-MAY-1999: 99US-0135629.
PR 25-MAY-1999: 99US-0136021.
PR 27-MAY-1999: 99US-0136392.
PR 28-MAY-1999: 99US-0136782.
PR 01-JUN-1999: 99US-0137222.
PR 03-JUN-1999: 99US-0137528.
PR 04-JUN-1999: 99US-0137502.
PR 07-JUN-1999: 99US-0137724.
PR 08-JUN-1999: 99US-0138094.
PR 10-JUN-1999: 99US-0138540.
PR 10-JUN-1999: 99US-0138847.
PR 14-JUN-1999: 99US-0139119.
PR 16-JUN-1999: 99US-0139452.
PR 16-JUN-1999: 99US-0139453.
PR 17-JUN-1999: 99US-0139492.
PR 18-JUN-1999: 99US-0139454.
PR 18-JUN-1999: 99US-0139455.
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Db	87	GKWCPLPG--SIVVATATNCCPPNNALANNNGWCMNPPEHFEDLAPVFORIAQYRAGIVP	144
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
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XX 06-SEP-2000.
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DT 17-OCT-2000 (first entry)
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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DB 79 GKWCPLPG--SIVYVATNCPNPNALANNNGGMCNPLHFDLAQVFPRIQYRAGIYV 136
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
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XX
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KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
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QY 67 TWCKRFGNSITITATNLCXPMWALPNSGCGNCPPLXHFDMSQPAMENIAVYQGIYVPV 126
DB 79 GWCCLPG--SIVTATNFCPPNNALANNNGCNPPLHFHDLAOFVFORIAQYRAGIYVPV 136
QY 127 NKRVXPORSIGIRFPAISHDYFELVTYTNVGSQVVAOMSIKGSNTGMMASRWGANW 186
DB 137 STRVPCRRRGIRFTINSHSYFNILVLTITNNGAGADYSAATKGSRTYVQAMSRWGMW 196
QY 187 QSNAYLAGOSISFTIVQLDGRKVTAMNXPXNM 219
DB 197 QSNSTYLNQALSFKVTTSQGRTVVSFNAAPAGM 229

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 PD 29-SEP-2000; 2000WO-US26884.
 XX 30-SEP-1999; 99US-0410191.
 PR (RECC) UNIV CALIFORNIA.
 PA Bradford KJ, Chen F, Dahal P, Downie B, Nonogaki H;
 PI MPI: 2001-266144/27.
 DR N-PSDB: AAD03712.
 XX Novel nucleic acid sequences isolated from germinating seeds encoding
 PT polypeptides that are useful to control seed germination in plants -
 PS Claim 3; Page 49; 63pp; English.
 CC The present invention relates to enzymes such as seed-specific
 CC endo-beta-mannanase (e.g., Lycopersicon esculentum (Lc) MAN2),
 CC polygalacturonase (PG) (e.g., LcXPG1), cellulases such as Cel5 and
 CC Cel68, arabinosidase (e.g., LcAR), xyloglucan endotransglycosylases
 CC (XET) (e.g., LcXET4) and expansins such as LcExp4, LcExp8 and LcExp10
 CC isolated from germinating seeds. All these enzymes are expressed
 CC initially in the endosperm caps and are associated with cell wall
 CC hydrolysis. These enzymes are associated with weakening of tissues
 CC surrounding the embryo and/or initiating radicle growth. The control of
 CC expression of these endogenous genes is therefore a convenient means for
 CC controlling seed germination. The present sequence is tomato seed
 CC expansin, LcExp8. Expansins are extracellular proteins that
 CC facilitate cell wall extension.
 XX Sequence 257 AA;
 SQ
 Query Match 63.9%; Score 765; DB 22; Length 257;
 Best Local Similarity 65.0%; Pred. No. 2,4e-70;
 Matches 139; Conservative 21; Mismatches 52; Indels 2; Gaps 2;

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 OY 66 QTKMCKPGCNSITITATNLCKXPMALPNSGCMNPPLXHFDMSPAMENIAVYQAGIIV 125
 DB 93 DPQMKCK-CVSTYITITSTNFCPPRYNLPSNNGCMCPRPRPHFDMQPAHEKIGIYKGIIV 151
 OY 126 VMYKRVYKQKSGIRFPAISGHDYFELVTVTVNGSGVYAQMSIKGNTGMAMSRNMGAN 185
 DB 152 VLYKRVCKKHGCVHFTINGRDYFELVTVSNVGAGSVESVQIKSNNTNWLMSRMGAS 211
 OY 166 WOSNAYLAGOSLSFTVQDDGKRYAMNXPX 219
 DB 212 WOSNAYLDGOSTSEKVTTSDDGVTFTPLNIPSSW 245

RESULT 6
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 AC 17-OCT-2000 (first entry)
 DT Arabidopsis thaliana protein fragment SFO ID NO: 3357.
 XX Arabidopsis thaliana
 DE Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS

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PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 20-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
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PR 06-AUG-1999; 99US-0147302.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151348.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152362.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153718.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.

XX 12-MAY-1994; 94AU-0068320.
 PF 12-MAY-1995; 95US-0440517.
 PR 12-MAY-1993; 93US-0060944.
 XX
 XX (PENN-) PENN STATE RES FOUND.
 XX Cosgrove DJ, McQueen-Mason S;
 PI WPI: 1996-201150/21.
 DR

XX Expansin proteins which alter the mechanical strength of
 PT poly:saccharide(s) - useful in paper mfr. and recycling
 XX
 XX Disclosure: Page 31-32; 60pp; English.
 PS

CC Expansins are a novel class of proteins that catalyse the extension
 CC of plant cell walls and the weakening of the hydrogen bonds in pure
 CC cellulose. 2 Expansins (AAR94528 and AAR94529) have been identified in
 CC rice and 3 in Arabidopsis (AAR94530-32). A cDNA clone (AAT13320)
 CC coding for cucumber expansin 29 (AAR94527) has been obtd. Expansins
 CC can be used e.g. in the mfr., de-linking and recycling of paper, in
 CC the textile industry, to aid delignification processes, to alter gel
 CC mechanical strength, etc.
 CC

SO Sequence 227 AA;

Query Match 98.4%; Score 1178; DB 17; Length 227;
 Best Local Similarity 100.0%; Pred. No. 8.3e-113;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KXSVQSAFAATFYGGKDSCTMGACGYGNLYNAGYGLYNALSSALFNDGAMGCACYTI 60
 DB 1 KXSVQSAFAATFYGGKDSCTMGACGYGNLYNAGYGLYNALSSALFNDGAMGCACYTI 60
 OY 61 TCDTQGTWCKCKGSGSITTTATNLCXPMWALPSNGSCNPLXHFDMQSOPAMENIAYQ 120
 DB 61 TCDTQGTWCKCKGSGSITTTATNLCXPMWALPSNGSCNPLXHFDMQSOPAMENIAYQ 120
 OY 121 AGIVPVNKRVPXORSRSGIRFAISGHDFELVTYTNVGSQVVAQMSIKGSNTGMMAMSR 180
 DB 121 AGIVPVNKRVPXORSRSGIRFAISGHDFELVTYTNVGSQVVAQMSIKGSNTGMMAMSR 180
 OY 181 NMGAMQSNAYLAGOSLSFTVQLDGRKVTAMNXPXNWL 220
 DB 181 NMGAMQSNAYLAGOSLSFTVQLDGRKVTAMNXPXNWL 220

RESULT 2

AAR94527
 ID AAR94527 standard; Protein: 227 AA.

AC AAR94527;

DT 08-JUL-1996 (first entry)

DE Cucumber expansin-29.

XX Expansin-29; plant cell wall; cellulose; paper recycling; de-linking;
 KW polysaccharide; cucumber.

OS Cucumis sativus var. Burpee Pickler.

XX A09540262-A.

PN 04-APR-1996.

PF 12-MAY-1994; 94AU-0068320.

PR 12-MAY-1995; 95US-0440517.
 PR 12-MAY-1993; 93US-0060944.

PA (PENN-) PENN STATE RES FOUND.

XX Cosgrove DJ, McQueen-Mason S;

XX WPI: 1996-201150/21.

DR N-PSDB; AAT13320.

XX Expansin proteins which alter the mechanical strength of
 PT poly:saccharide(s) - useful in paper mfr. and recycling

PS Claim 7; Page 30; 60pp; English.

CC Cucumber expansin-29 (AAR94527) is a member of a novel class of
 CC proteins that catalyse the extension of plant cell walls and the
 CC weakening of the hydrogen bonds in pure cellulose. It can be obtd.
 CC by expression of an isolated cDNA clone (see AAT13320) in bacterial or
 CC other host cells. Expansin proteins have also been identified in oat
 CC coleoptiles, in Arabidopsis (see AAR94530-32) and in rice (AAR94528-29),
 CC and appear to be broadly distributed throughout the plant kingdom.
 CC Expansins can be used e.g. in the mfr., de-linking and recycling of
 CC paper, in the textile industry, to aid delignification processes, to
 CC alter gel mechanical strength, etc.
 CC

SO Sequence 227 AA;

Query Match 64.6%; Score 773.5; DB 17; Length 227;
 Best Local Similarity 64.5%; Pred. No. 2.8e-71;
 Matches 138; Conservative 27; Mismatches 46; Indels 3; Gaps 2;

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 DB 6 QSHATFYGGGSDASGTMGACGYGNLYSGYGTNTVALSTALPNNGLSCACACEMTC-TN 64
 OY 66 QTKCKRGSGSITTTATNLCXPMWALPSNGSCNPLXHFDMQSOPAMENIAYQAGIYP 125
 DB 65 DPKWCLPG--TIRVTATNFCPPNFALPNNNGGWCNPLQHFDAEPFLQIAQYRAGIYP 122
 OY 126 VNYKRVXORSRSGIRFAISGHDFELVTYTNVGSQVVAQMSIKGSNTGMMAMSRMGMAN 185
 DB 123 VSRFRVPCMKKGGRFTINHSYFNLYLTITNVGAGAGVHSYIKGSRITGQMSRMGMON 182
 OY 186 WQSNAYLAGOSLSFTVQLDGRKVTAMNXPXNWL 219
 DB 183 WQSNAYLAGOSLSFTVQLDGRKVTAMNXPXNWL 216

RESULT 3

AAG26696
 ID AAG26696 standard; Protein: 252 AA.

AC AAG26696;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 31249.

XX Protein identification: signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

OS Arabidopsis thaliana.

XX EPI033405-A2.

PN 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:49:55 ; Search time 25.1292 Seconds
(without alignments)
1003.367 Million cell updates/sec

Title: US-09-896-301-4

Perfect score: 1197
Sequence: 1 KXSVASAPAFYFGKDGSC.....KVTAMNAPXNLXXXXXX 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	773.5	64.6	227 17 AAR94527	Cucumber expansin
3	766	64.0	252 21 AAG26696	Arabidopsis thalia
4	766	64.0	266 21 AAG26695	Arabidopsis thalia
5	765	63.9	257 22 AAE00413	Tomato seed expans
6	744.5	62.2	241 21 AAG06546	Arabidopsis thalia
7	744.5	62.2	241 21 AAG51633	Arabidopsis thalia
8	744.5	62.2	241 21 AAG51647	Arabidopsis thalia
9	744.5	62.2	249 21 AAG06545	Arabidopsis thalia
10	744.5	62.2	249 21 AAG51632	Arabidopsis thalia
11	744.5	62.2	249 21 AAG51646	Arabidopsis thalia

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13	744.5	62.2	259 21 AAG51631	Arabidopsis thalia
14	744.5	62.2	280 21 AAG51645	Arabidopsis thalia
15	742	62.0	227 17 AAR94532	Arabidopsis expans
16	740.5	61.9	250 22 AAE00414	Tomato seed expans
17	733.5	61.3	228 17 AAR94528	Rice expansin. Or
18	732.5	61.2	257 21 AAG36445	Arabidopsis thalia
19	731.5	61.1	251 21 AAG23852	Arabidopsis thalia
20	731.5	61.1	251 21 AAG43343	Arabidopsis thalia
21	731.5	61.1	253 21 AAG23851	Arabidopsis thalia
22	731.5	61.1	253 21 AAG43342	Arabidopsis thalia
23	731.5	61.1	281 21 AAG43341	Arabidopsis thalia
24	731.5	61.1	282 21 AAG23850	Arabidopsis thalia
25	727.5	60.8	262 21 AAG29931	Arabidopsis thalia
26	727.5	60.8	273 21 AAG29930	Arabidopsis thalia
27	725.5	60.6	255 21 AAG30325	Arabidopsis thalia
28	725.5	60.6	257 21 AAG30324	Arabidopsis thalia
29	719.5	60.1	263 22 AAE00412	Tomato seed expans
30	718	60.0	210 21 AAG26697	Arabidopsis thalia
31	702.5	58.7	250 21 AAG09622	Arabidopsis thalia
32	702.5	58.7	258 21 AAG09621	Arabidopsis thalia
33	702.5	58.7	280 21 AAG09620	Arabidopsis thalia
34	701.5	58.6	241 21 AAG05453	Arabidopsis thalia
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36	701.5	58.6	255 21 AAG05451	Arabidopsis thalia
37	701	58.6	253 21 AAG25443	Arabidopsis thalia
38	701	58.6	253 21 AAG25443	Arabidopsis thalia
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41	700.5	58.5	255 21 AAG36568	Arabidopsis thalia
42	678	56.6	185 21 AAG27400	Arabidopsis thalia
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44	677.5	56.6	210 21 AAG36446	Arabidopsis thalia
45	673.5	56.3	210 21 AAG30326	Arabidopsis thalia

ALIGNMENTS

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AA94530	standard; Protein; 227 AA.
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AC	AA94530;
XX	
DT	08-JUL-1996 (first entry)
XX	
DE	Arabidopsis expansin.
XX	
KW	Expansin; plant cell wall; cellulose; paper recycling; de-inking;
KW	polysaccharide.
XX	
OS	Arabidopsis sp.
XX	
FH	Key
FT	Misc-difference 2
FT	/note= "unidentified amino acid"
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FT	Misc-difference 104
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PN	AU9540262-A.
XX	
PD	04-APR-1996.

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QY	7	SAPFTFYAGKGGSCCTMGAGCGYGNLYNAAAGYGLYNAAALSALFENDGACGACCTTCTC	66
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QY	67	TKWCKPGGNSITTTATNLCXPHMALPSNSGWCNPLXHFDMDSOPAMENIAYVQAQIVPV	126
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QY	127	NYKRYPAORSGCIGRPALISGHDYFELYVTYTNVGGSGVYAQMSIGKSNITGNMAAMSRNMGAN	166
Db	117	MYRRARCRSGGIGFTINGHSYFNLYVTYNVGGAGDVHSVMKSGRTRKWLMSRNMGNM	176
QY	187	QSNAYLAGOSLSFYVLDGGRKRYAMNXPXNM	219
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RESULT 13
US-09-092-160--3
Sequence 3 Application US/09092160C
Patent NO. 6255466
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guillian, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114053
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 222
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: rice expansin
NAME/KEY: UNSURE
LOCATION: (14)..(58)
OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160--3

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[illegible]

RESULT 14

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US-08-845-539-6
: Sequence 6, Application US/08845539
: Patent No. 5929303
: GENERAL INFORMATION:
: APPLICANT: Bennett, Alan B.
: APPLICANT: Rose, Jocelyn K.C.
: TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
: TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/845,539
: FILING DATE: 25-APR-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Bastian, Kevin L.
: REGISTRATION NUMBER: 34,774
: REFERENCE/DOCKET NUMBER: 023070-078200US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 179 amino acids
: TYPE: amino acid
: TOPOLOGY: Linear
: MOLECULE TYPE: protein
: US-08-845-539-6

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[illegible]

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: RESULT 15
: US-09-362-642-6
: Sequence 6, Application US/09362642
: Patent No. 6350935
: GENERAL INFORMATION:
: APPLICANT: Bennett, Alan B.
: APPLICANT: Rose, Jocelyn K.C.
: TITLE OF INVENTION: The Regents of the University of California
: TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
: FILE REFERENCE: 023070-078210US
: CURRENT APPLICATION NUMBER: US/09/362,642
: CURRENT FILING DATE: 1999-07-27
: NUMBER OF SEQ. ID NOS.: 8
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 6

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APPLICANT: Gullinan, Mark J
APPLICANT: Shcherban, Tatyana
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C11A053
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 225
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
US-09-092-160-5

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Best local Similarity 57.8%; Score 660.5; DB 4; Length 225;
Matches 122; Conservative 33; Mismatches 49; Indels 7; Gaps 4;

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QY 189 NAYLAGOSLSFIVQLDGRKRVTAANXAPXNM 219
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RESULT 11
US-08-845-539-2
Sequence 2, Application US/0845539
Patent No. 5929303
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/845,539
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-078200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-845-539-2

Query Match
Best local Similarity 59.4%; Score 658.5; DB 2; Length 225;
Matches 114; Conservative 32; Mismatches 45; Indels 1; Gaps 1;

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RESULT 12
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Sequence 3, Application US/08440517A
Patent No. 5959082
GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GULLINAN, MARK;
APPLICANT: SCHERBAN, TATYANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
ADDRESS: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 222
TYPE: AMINO ACID
TOPOLOGY: UNKNOWN
US-08-440-517A-3

Query Match
Best local Similarity 54.2%; Score 649; DB 2; Length 222;
Matches 123; Conservative 25; Mismatches 55; Indels 10; Gaps 3;

QY 181 MWGANMOSNAYLAGOSLSFTIYOLDGRRKVTAMNXPXNML 220
Db 181 MWGANMOSNAYLAGOSLSFTIYOLDGRRKVTAMNXPXNML 220

RESULT 2

US-09-092-160-4
Sequence 4, Application US/09092160C
Patent No. 6255466
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Gullitman, Mark J
APPLICANT: Shcherban, Tatyana
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 227
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
FEATURE:
NAME/REV: UNSURE
LOCATION: (2)..(227)
OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160-4

Query Match 98.4%: Score 1178; DB 4; Length 227;
Best Local Similarity 100.0%: Pred No. 3.2e-107;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXSVAGAFATFYGGKDGSCCTMGACGYNLVYAGYGLYNAALSSALFNDGAMGACYYTI 60
Db 1 KXSVAGAFATFYGGKDGSCCTMGACGYNLVYAGYGLYNAALSSALFNDGAMGACYYTI 60
QY 61 TCDFSTQKWKCKPGGNSITITATNLCXPNMALPNSGSGWCNPLXHPDMSQPAVENTAVYQ 120
Db 61 TCDFSTQKWKCKPGGNSITITATNLCXPNMALPNSGSGWCNPLXHPDMSQPAVENTAVYQ 120
QY 121 AGIVPVYKRVXQSGIRFPAISGHDYFELVTVTNVGGSGVVAQMSIKSNTGMMAMSR 180
Db 121 AGIVPVYKRVXQSGIRFPAISGHDYFELVTVTNVGGSGVVAQMSIKSNTGMMAMSR 180
QY 181 MWGANMOSNAYLAGOSLSFTIYOLDGRRKVTAMNXPXNML 220
Db 181 MWGANMOSNAYLAGOSLSFTIYOLDGRRKVTAMNXPXNML 220

RESULT 3

US-09-092-160-7
Sequence 7, Application US/09092160C
Patent No. 6255466
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Gullitman, Mark J
APPLICANT: Shcherban, Tatyana
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 227
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cucurbit
US-09-092-160-7

Query Match 64.1%: Score 767.5; DB 4; Length 227;
Best Local Similarity 64.0%: Pred No. 2.9e-67;
Matches 137; Conservative 27; Mismatches 47; Indels 3; Gaps 2;

QY 6 QSAFATFYGGKDGSCCTMGACGYNLVYAGYGLYNAALSSALFNDGAMGACYYTIYCDTS 65
Db 6 QSAFATFYGGKDGSCCTMGACGYNLVYAGYGLYNAALSSALFNDGAMGACYYTIYCDTS 65
QY 66 QPKWCKPGGNSITITATNLCXPNMALPNSGSGWCNPLXHPDMSQPAVENTAVYQAGIVP 125
Db 66 QPKWCKPGGNSITITATNLCXPNMALPNSGSGWCNPLXHPDMSQPAVENTAVYQAGIVP 125
QY 126 VNKRRVXQSGIRFPAISGHDYFELVTVTNVGGSGVVAQMSIKSNTGMMAMSRMNGAN 185
Db 126 VNKRRVXQSGIRFPAISGHDYFELVTVTNVGGSGVVAQMSIKSNTGMMAMSRMNGAN 185
QY 186 WOSNAYLAGOSLSFTIYOLDGRRKVTAMNXPXNML 219
Db 186 WOSNAYLAGOSLSFTIYOLDGRRKVTAMNXPXNML 219

US-08-440-517A-6
Sequence 6, Application US/08440517A
Patent No. 5959082
GENERAL INFORMATION:

APPLICANT: COSGROVE, DANIEL J.,
APPLICANT: GULLITMAN, MARK,
APPLICANT: SCHERBAN, TATYANA;
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 226
TYPE: AMINO ACID

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:54:05 ; Search time 8.87897 Seconds
(without alignments)
624.466 Million cell updates/sec

Title: US-09-896-301-4

Perfect score: 1197
Sequence: 1 KXSVASAFATFYGGKDGSC.....KYTAMNAXAPXNWLXXXXXX 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
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3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCFUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1178	98.4	227	US-08-440-517A-4	Sequence 4, Appl1
2	1178	98.4	227	US-09-092-160-4	Sequence 4, Appl1
3	767.5	64.1	227	US-09-092-160-7	Sequence 7, Appl1
4	742	62.0	226	US-08-440-517A-6	Sequence 6, Appl1
5	742	62.0	226	US-09-092-160-6	Sequence 6, Appl1
6	733.5	61.3	228	US-08-440-517A-2	Sequence 2, Appl1
7	733.5	61.3	228	US-09-092-160-2	Sequence 2, Appl1
8	663.5	55.4	225	US-09-362-642-2	Sequence 2, Appl1
9	660.5	55.2	225	US-08-440-517A-5	Sequence 5, Appl1
10	660.5	55.2	225	US-09-092-160-5	Sequence 5, Appl1
11	658.5	55.0	225	US-08-845-539-2	Sequence 2, Appl1
12	649	54.2	222	US-08-440-517A-3	Sequence 3, Appl1
13	649	54.2	222	US-09-092-160-3	Sequence 3, Appl1
14	627.5	52.4	179	US-08-845-542-6	Sequence 6, Appl1
15	627.5	52.4	179	US-09-362-642-6	Sequence 6, Appl1
16	576.5	48.2	167	US-08-845-539-4	Sequence 4, Appl1
17	576.5	48.2	167	US-09-362-642-4	Sequence 4, Appl1
18	180.5	15.1	261	US-07-971-096-2	Sequence 2, Appl1
19	180.5	15.1	261	US-08-175-096-2	Sequence 2, Appl1
20	169.5	14.2	263	US-07-971-096-4	Sequence 4, Appl1
21	169.5	14.2	263	US-08-175-096-4	Sequence 4, Appl1
22	169.5	14.2	263	US-08-413-974-6	Sequence 6, Appl1
23	169.5	14.2	263	US-08-434-418-6	Sequence 6, Appl1
24	169.5	14.2	263	US-08-433-288-6	Sequence 6, Appl1
25	169.5	14.2	263	US-08-174-739A-6	Sequence 6, Appl1
26	165	13.8	246	US-08-441-507-21	Sequence 21, Appl1
27	165	13.8	272	US-08-441-507-15	Sequence 15, Appl1

28	160	13.4	245	4	US-08-441-507-24	Sequence 24, Appl1
29	125.5	10.5	197	4	US-08-441-507-5	Sequence 5, Appl1
30	125.5	10.5	200	4	US-08-441-507-4	Sequence 4, Appl1
31	107.5	9.0	122	4	US-08-441-507-23	Sequence 23, Appl1
32	92.5	7.7	213	5	PCT-US96-09848-21	Sequence 21, Appl1
33	92.5	7.7	314	5	US-08-486-036A-4	Sequence 4, Appl1
34	92.5	7.7	314	5	PCT-US96-09848-4	Sequence 4, Appl1
35	92.5	7.7	356	5	PCT-US96-09848-24	Sequence 24, Appl1
36	92.5	7.7	398	1	US-08-486-036A-2	Sequence 2, Appl1
37	92.5	7.7	398	1	PCT-US96-09848-2	Sequence 2, Appl1
38	90.5	7.6	316	5	US-08-482-282B-4	Sequence 4, Appl1
39	90.5	7.6	400	1	US-08-482-282B-2	Sequence 2, Appl1
40	83.5	7.0	145	4	US-08-413-974-4	Sequence 4, Appl1
41	83.5	7.0	145	4	US-08-434-418-4	Sequence 4, Appl1
42	83.5	7.0	145	4	US-08-433-288-4	Sequence 4, Appl1
43	83.5	7.0	145	4	US-08-174-739A-4	Sequence 4, Appl1
44	82.5	6.9	284	1	US-08-411-777-10	Sequence 10, Appl1
45	82.5	6.9	284	3	US-09-057-088-10	Sequence 10, Appl1

ALIGNMENTS

```

RESULT 1
US-08-440-517A-4
; Sequence 4, Application US/08440517A
; Patent No. 5959082
; GENERAL INFORMATION:
; APPLICANT: COSGROVE, DANIEL J.;
; APPLICANT: GUILTINAN, MARK;
; APPLICANT: SHCHERBAN, TATYANA;
; APPLICANT: SHI, JUN
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
; ADDRESS: PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,517A
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
; US-08-440-517A-4

Query Match          98.4%; Score 1178; DB 2; Length 227;
Best local similarity 100.0%; Pred. No. 3.2e-107;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 185 WMSNAYLAGOSLSFTVOLDGGRKVTAMNXPXNM 219
 Db 217 WMSNAYLAGOSLSFTVOLDGGRKVTAMNXPXNM 251

RESULT 13 T06573

expansin 18 - tomato
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
 C:Accession: T06573
 R:Reinhardt, D.; Wiltner, F.; Mandel, T.; Kuhlmeier, C.
 submitted to the EMBL Data Library, March 1998
 A:Description: Localized up-regulation of a new expansin gene predicts the site of leaf
 A:Reference number: 215768
 A:Accession: T06573
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-255 <REI>
 A:Cross-references: EMBL:AJ004997; PIDN:CAA06271.1
 A:Experimental source: cultivar Money Maker
 C:Genetics:
 A:Gene: exp18
 C:Superfamily: expansin

Query Match 61.7%; Score 738.5; DB 2; Length 255;
 Best Local Similarity 61.7%; Pred. No. 2,7e-56;
 Matches 132; Conservative 30; Mismatches 51; Indels 1; Gaps 1;

QY 6 OSATFATFYGGKDGSCITMGACGYGLYNAGYLNALSSALFNDGAMGACACTTTCDS 65
 Db 30 OSATFATFYGGSDASGTMGACGYGLYNAGYLNALSSALFNDGAMGACACTTTCDS 88
 QY 66 QTKWCKPGGNSITTTATNLCXRNMAIPNSGCGWCPPLXHPDMSOPAMENIAVYQAGIYP 125
 Db 89 YPQWCHPGSPSIFITATNCPNFPALPNDGWCMPRPHFLAMPFLHAEYRAGIYP 148
 QY 126 VVKRVPXORSRGIRFPAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGMMAMSRMNGAN 185
 Db 149 VYRRPCKRGKGGIRFTINGFRFNLVLTNVAAGADISLSIKSKTNWISMRMNGON 208
 QY 186 WOSNAYLAGOSLSFTVOLDGGRKVTAMNXPXNM 219
 Db 209 WQTNVYLFQGSLSFRVRADRRSSTSMITPAHW 242

RESULT 14 T09825

expansin (clone pTexp4) - loblolly pine (fragment)
 C:Species: Pinus taeda (loblolly pine)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
 C:Accession: T09825
 R:Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
 submitted to the EMBL Data Library, July 1996
 A:Description: Expansins are conserved in conifers and expressed in response to exogenous
 A:Reference number: 216866
 A:Accession: T09825
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-232 <HUT>
 A:Cross-references: EMBL:U64892; NID:91778102; PID:91778103
 A:Experimental source: clone pTexp4
 C:Superfamily: expansin

Query Match 61.6%; Score 737.5; DB 2; Length 232;
 Best Local Similarity 63.1%; Pred. No. 3e-56;
 Matches 135; Conservative 24; Mismatches 52; Indels 3; Gaps 2;

QY 6 OSATFATFYGGKDGSCITMGACGYGLYNAGYLNALSSALFNDGAMGACACTTTCDS 65
 Db 11 OSATFATFYGGSDASGTMGACGYGLYNAGYLNALSSALFNDGAMGACACTTTCDS 69
 QY 66 QTKWCKPGGNSITTTATNLCXRNMAIPNSGCGWCPPLXHPDMSOPAMENIAVYQAGIYP 125

Db 70 DPQWCLPG--VTITATNCPNFPALPNDGWCMPPLPHDPMAPLAKYRGGIYP 127
 QY 126 VVKRVPXORSRGIRFPAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGMMAMSRMNGAN 185
 Db 128 ILYTRVPCIRKGGIRFTVNGHSCFNLVLTNVAAGADVHVASIKGPRSGWQPMRNMNGON 187
 QY 186 WOSNAYLAGOSLSFTVOLDGGRKVTAMNXPXNM 219
 Db 188 WOSNAYLAGOSLSFTVOLDGGRKVTAMNXPXNM 221

RESULT 15 T10083

expansin S2 precursor - cucumber
 C:Species: Cucumis sativus (cucumber)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T10083
 R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gullitlan, M.J.; McQueen-Mason, S.J.; Shi
 Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
 A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
 A:Reference number: 214894; MUID:96016146
 A:Accession: T10083
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-258 <SHC>
 A:Cross-references: EMBL:U03460; NID:91040876; PIDN:AAB37749.1; PID:91040877
 A:Experimental source: cv. Burpee Pickler; hypocotyl
 C:Genetics:
 A:Gene: Exp2
 C:Function:
 A:Description: induces cell wall extension in plants
 C:Superfamily: expansin
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-258/Product: expansin #status predicted <MAT>

Query Match 61.5%; Score 736.5; DB 2; Length 258;
 Best Local Similarity 61.7%; Pred. No. 4.1e-56;
 Matches 132; Conservative 28; Mismatches 51; Indels 3; Gaps 3;

QY 8 AFATFYGGKDGSCITMGACGYGLYNAGYLNALSSALFNDGAMGACACTTTCDS-TSQ 66
 Db 33 AHATFYGGSDASGTMGACGYGLYNAGYLNALSSALFNDGAMGACACTTTCDS 92
 QY 67 TKWCKPGGNSITTTATNLCXRNMAIPNSGCGWCPPLXHPDMSOPAMENIAVYQAGIYP 126
 Db 93 PRWCIRKA-SVITATNCPNFPALPNDGWCMPRPHFLAMPFLHAEYRAGIYP 151
 QY 127 VVKRVPXORSRGIRFPAISGHDYFELVTVTNVGGSGVVAQMSIKGS-NTGMMAMSRMNGAN 185
 Db 152 LYQRPCKRGKGGIRFTVNGHSCFNLVLTNVAAGADISLSIKSKTNWISMRMNGON 211
 QY 186 WOSNAYLAGOSLSFTVOLDGGRKVTAMNXPXNM 219
 Db 212 WQSNAYLAGOSLSFTVOLDGGRKVTAMNXPXNM 245

Search completed: October 11, 2002, 15:01:00
 Job time : 12.3919 secs

[illegible]

RESULT 6
T09821
expansin (clone ptxep3) - loblolly pine (fragment)
C:Species: Pinus taeda (loblolly pine)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09821
R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09821
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64891; NID:g1778100; PID:g1778101
A:Experimental source: clone ptxep3
C:Superfamily: expansin

[illegible]

RESULT 7
T09826
expansin (clone ptxep5) - loblolly pine (fragment)
C:Species: Pinus taeda (loblolly pine)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09826
R:Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09826
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-References: EMBL:U64893; NID:q1778104; PID:q1778105

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A:Experimental source: clone ptxexp5
C:Superfamily: expansin

Query Match      62.7%  Score 750.5  DB 2:  Length 232:
Best Local Similarity 63.6%  Pred. No. 2.3e-57:
Matches 136: Conservative 25: Mismatches 50: Indels 3: Gaps 2:

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QY	6	OSAFETFFVGGKDGSCOTMAGACGYENLNAAGLNAALSSALFEDGAMGACVTTIDIS	63
Db	11	ESAAHTFFVGGSDASTMAGACGYENLISQGTGTALSTALFNDGLSCACACVEMQCN-D	69
QY	66	QTRKCKPGGNSITTTATNLCKPNNALDSNSGWCNCPPLXHFDMSQPAMENIANYQAGIVP	125
Db	70	DPQWCLPG-FVTVAATNFCPPNNALPDDNGMGNCPLOHEDMAEPALFIARRGIVP	127
QY	126	VNYKRVPPQORSQGIREFALSGHDYFELYVTNVGSSGYAQMSTKGSUTGMAMSRNNGA	185
Db	128	ILYTVPECLRRKGJREFYVNGSHYFNLVITTVNGAGADVNAVSLKGRSGQMPMSRNNGN	187
QY	166	WQSNAYLAGOSLSFVQLDDSRKVTAMNAXEYXW	219
Db	188	WQSNSTYLGOSLSFQVYTTSDGRVTYVSNNAVSNW	221

RESULT 8
 T09818
 expansin (clone ptxexp2) - loblolly pine (fragment)
 C:Species: Pinus taeda (loblolly pine)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
 C:Accession: T09818
 R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
 submitted to the EMBL Data Library, July 1996
 A:Description: Expansins are conserved in conifers and expressed in response to exogen
 A:Reference number: Z16856
 A:Accession: T09818
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-232 <NR>
 A:Cross-references: EMBL:U64890; NID:q1778098; PID:q1778099
 A:Experimental source: clone ptxexp2; hypocotyl
 C:Superfamily: expansin

[illegible]

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RESULT 9
T50658
expansin 9 [imported] - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C:Accession: T50658
R:Caderas, D.M.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z25160
A:Accession: T50658

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:53:05 ; Search time 11.3919 Seconds
(without alignments)
1914.721 Million cell updates/sec

Title: US-09-896-301-4

Perfect score: 1197

Sequence: 1 KXSAQSAFAATFYGGKDGSC.....KVTAMNAPXNMLXXXXXX 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173	98.0	255	2	T03299
2	773.5	64.6	250	2	T10079
3	764.5	63.9	252	2	F86335
4	762.5	63.7	251	2	T03298
5	756	63.2	261	2	T03737
6	750.5	62.7	232	2	T09821
7	747.5	62.7	232	2	T09826
8	747.5	62.4	232	2	T09818
9	746.5	62.4	257	2	T50658
10	746.5	62.4	260	2	T47689
11	743.5	62.1	246	2	T04175
12	742.5	62.0	264	2	T50659
13	738.5	61.7	255	2	T06573
14	737.5	61.6	232	2	T09825
15	736.5	61.5	258	2	T10083
16	733.5	61.3	237	2	T50634
17	733.5	61.3	262	2	T50660
18	731.5	61.1	257	2	D84820
19	731.5	61.1	248	2	C84444
20	731.5	61.1	258	2	S53082
21	727.5	60.8	262	2	T02530
22	725.5	60.6	257	2	T02727
23	725.5	60.6	259	2	T50653
24	721.5	60.3	261	2	T07630
25	709.5	59.3	258	2	T09786
26	707.5	59.1	260	2	T08016
27	702.5	58.7	258	2	T48247
28	702	58.6	253	2	T50656
29	701	58.6	253	2	F84831

30	692.5	57.9	255	2	T02010	expansin homolog T
31	670	56.0	255	2	T50655	expansin EXP5 [imp
32	626.5	52.3	257	2	F86259	protein T12C24.10
33	600.5	50.2	257	2	G96654	hypothetical prote
34	513	42.9	160	2	T09871	expansin - upland
35	503.5	42.1	256	2	T05648	expansin homolog F
36	233	19.5	491	2	F96681	protein F1R22.6 [i
37	229.5	19.2	259	2	T50657	beta-expansin [imp
38	229.5	19.2	271	2	H84592	beta-expansin [imp
39	221	18.5	259	2	E84886	probable beta-expa
40	219	18.3	77	2	T09815	expansin (clone pd
41	217	18.1	102	2	T09828	expansin (clone pp
42	213.5	17.8	277	2	S48032	ciml protein - soy
43	207.5	17.3	276	2	T09041	ciml protein homol
44	199	16.6	81	2	T09830	expansin (clone pp
45	197.5	16.5	261	2	T04301	beta-expansin - r1

ALIGNMENTS

RESULT 1
T03299
expansin 3 - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03299
R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Nason, S.J.; Shi
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
A:Reference number: Z14894; MUID:96016146
A:Accession: T03299
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-255 <SHC>
A:Cross-references: EMBL:U030479; NID:g1041711; PIDN:AAB38075.1; PID:g1041712
C:Genetics:
A:Gene: EXP3
C:Function:
A:Description: induces extension (creep) in plant cell walls
C:Superfamily: expansin

Query Match 98.0%; Score 1173; DB 2; Length 255;
Best Local Similarity 97.7%; Pred. No. 11e-93;
Matches 214; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KXSAQSAFAATFYGGKDGSCITMGACGYGNDLYNMGYGLYNALSSALFNDGACGACTT 60
|||||
Db 24 KXSAQSAFAATFYGGKDGSCITMGACGYGNDLYNMGYGLYNALSSALFNDGACGACTT 83

QY 61 TCDTSQITWCKRPGGSGITTTATNLCXPMWALPNSGCGNPLXHFMSQPAWENIAYVQ 120
|||||
Db 84 TCDTSQITWCKRPGGSGITTTATNLCXPMWALPNSGCGNPLXHFMSQPAWENIAYVQ 143

QY 121 AGIYVNNKRVXORSGIRFASGHDFELVTYNNVGGSGVVAOMSTKSGNTGMAMSR 180
|||||
Db 144 AGIYVNNKRVXORSGIRFASGHDFELVTYNNVGGSGVVAOMSTKSGNTGMAMSR 203

QY 181 NWGANWQSNAYLAGQSLSFIVQDDGKRKVTAMNAPXNWX 219
|||||
Db 204 NWGANWQSNAYLAGQSLSFIVQDDGKRKVTAMNAPXNWX 242

RESULT 2
T10079
expansin S1 precursor - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T10079
R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Nason, S.J.; Shi
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
A:Reference number: Z14894; MUID:96016146

RESULT 15

ENV2_MOUSE ID ENV2_MOUSE STANDARD; PRT; 432 AA.
 AC P11370;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, last sequence update)
 DT 01-NOV-1991 (Rel. 20, last annotation update)
 DE Retrovirus-related ENV polypeptide (FV-4 locus) (Fragments).
 GN ENV.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85265041; PubMed=2991595;
 RA Ikeda H., Laigret F., Martin M.A., Repaske R.;
 RT "Characterization of a molecularly cloned retroviral sequence
 RT associated with Fv-4 resistance."
 RL J. Virol. 55:768-777(1985).
 CC -----
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 CC -----
 DR EMBL: M11051; AAA37562.1; -
 DR EMBL: M11052; AAA37563.1; -
 DR PIR: A25483; A25483.
 DR HSSP: P03390; IAOI.
 DR Pfam: PF00429; ENV_polypeptide; 1.
 KW Coat protein; Polypeptide.
 FT NON_CONS 348 349
 SQ SEQUENCE 432 AA; 47661 MW; 092D3963EE5771FC CRC64;

Query Match

Best Local Similarity 7.1%; Score 84.5; DB 1; Length 432;
 Matches 29; Conservative 10; Mismatches 37; Indels 27; Gaps 5;

QY 54 CGA-----CYTTCDFRSGTKCKCPGNSITIT-ATNLCKPNNALPNSGWCNPLXHD 107
 DB 164 CGCPKAYTCASGCGCTTGRAAKPTISSMDYITVSNLSSPOAFKACKKNGCNPLVRF- 222
 QY 108 MSQPAWENIAVYQAGIVPNYKRPVXORSG---GIRFAISGHD 147
 DB 223 -TGPG-----KRATSWTGTGHEWGLRLYISGHD 248

Search completed: October 11, 2002, 14:57:32
 Job time : 7.86347 secs

FT	CARBONHYD	430	430	N-LINKED (GLCNAC...)	(POTENTIAL).
CD	NON_TER	534	534		
SO	SEQUENCE	534 AA;	58348 MW;	D3A50B10B7F22BB3	CRC64;
Query Match					
Best Local Similarity		7.1%;	Score 85.5;	DB 1;	Length 534;
Matches 34;		Conservative 15;	Mismatches 44;	Indels 65;	Gaps 6;
Oy	14	GKDGSCITMGAGACGYCNLY-----	-----	-----	-----
		: : : : : : : :			
Db	126	GPDGDFCAVWGCGTTEGYTWPRPTSSMDITYAKKGYTGQIYC-----	-----	-----	-----
		: : : : : : : :			
Oy	60	ITCDQSOTKWCXPGKNSITITATNLCXPNMALPSNSGCMCPNPLXHPDMS--OPAWENIA	117		
		: : : : : : : :			
Db	179	-----KAVHSSIT-----	-----	-----	-----
		: : : : : : : :			
Oy	118	VYQAGTIVPVKKRVKQSGRIKFAISGHDYFELTWT	155		
		: : : : : : : :			
Db	213	-----PKSMGRLRLTRSGIDPLALPSVS	234		

ID	ENV_FLVLB	STANDARD:	PRF:	662 AA.
AC	P11261; 085515; 085516; 085517;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-JUL-1989 (Rel. 11, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	ENV polypeptide precursor (Coat polypeptide) [Contains: knob protein			
DE	GP70; Spike protein P156] (Fragment).			
ENV				
OS	Feline leukemia virus (strain B/Jambda-B1).			
OC	Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.			
OX	NCBI_TaxID=103916;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88036192; PubMed=2444714;			
RA	Nicolaissen-Strouss K., Kumar H.P.M., Elting T., Grant C.K.,			
RA	Elder J.H.;			
RT	"Natural feline leukemia virus variant escapes neutralization by a			
RT	monoclonal antibody via an amino acid change outside the antibody-			
RT	binding epitope."			
RL	J. Virol. 61:3410-3415(1987).			
CC	-1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.			
CC				
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CC	or send an email to license@isb-sib.ch).			
CC				
CC	EMBL: J03448; AAA3048.1; -			
DR	PIR: A27172; VCNVLB.			
DR	HSSP: P03385; TMOF.			
DR	InterPro: IPR002050; Env_polypeptide.			
DR	Pfam: PF00429; Env_polypeptide. 1.			
KW	Coat protein; Glycoprotein; Polypeptide; Signal.			
FT	SIGNAL	1	33	
FT	CHAIN	34	465	
FT	CHAIN	466	662	
FT	CARBOHYD	43	43	
FT	CARBOHYD	58	58	
FT	CARBOHYD	286	286	
FT	CARBOHYD	322	332	
FT	CARBOHYD	327	337	
FT	CARBOHYD	351	351	
FT	CARBOHYD	354	354	
FT	CARBOHYD	430	430	
FT	NON_TER	662	662	
QO	SEQUENCE	662 AA;	73132 MW;	DAAC18E197230575 CRC64;

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Query Match: 7.1%; Score 85.5; DB 1; Length 662;
Best Local Similarity 21.5%; Pred. No. 2.8;
Matches 34; Conservative 15; Mismatches 44; Indels 65; Gaps 6.

QY 14 GKGDSCTMGACGCGYGLY-----NAGYGLYNAALSSALFPDAGMCAGCYT 59
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 126 GPDGDFCAVWGCGTTFETFYMRPTSSMDYITVKKGYTQIYGC-----SGGMCAGCYT 178
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 60 ITCDTSOTKWKCKGCGSITITTTATNLCPXNALPSNSGCMCPPLXHPDMS--QPAENIA 117
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 179 -----KAVHSSIT-----GASEGCRCPDLIQETOKGRQTSWDC-- 212
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 118 VYQAGIVPVNKKRVKQXSGGIRFPAISGDHYFELTYT 155
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 213 -----PKSMGRLRLRGSGTDPLALFVS 214
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 14	STANDARD:	PRF:	181 AA.
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Endoglycanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (cellulase) (CMCase).		
OS	Mytilus edulis (Blue mussel).		
OC	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida; Mytiloidae; Mytilidae; Mytilus.		
OX	NCBI_TaxId=6550;		
RN	[1]		
RP	SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.		
RC	TISSUE-Digestive gland:		
RA	MEDLINE=20389517; PubMed=10931178.		
RX	Xu B, Hellman U, Ersson B, Janson J.-C.:		
RT	"Purification, characterization and amino acid sequence analysis of a thermolabile, low molecular mass endo-beta-1,4-glucanase from blue mussel, Mytilus edulis."		
RL	Eur. J. Biochem. 267:4970-4977(1999).		
CC	-1- FUNCTION: ACTIVE TOWARDS THE SOLUBLE CARBOXYMETHYLCELLULOSE (CMC). POSSESSES EXPANSIN ACTIVITY TOO.		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose.		
CC	-1- TISSUE SPECIFICITY: DIGESTIVE GLAND.		
CC	-1- MASS SPECTROMETRY: MW=19702; METHOD=MALDI.		
CC	-1- MISCELLANEOUS: Has an isoelectric point of 7.6. Its optimum pH is 4.6 and optimum temperature is between 30-50 degrees Celsius.		
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL HYDROLASES).		
DR	InterPro: IPR000334; Glyco_hydro.45.		
DR	ProSITE: PS01140; GLYCOSYL_HYDROL_F45; FALSE NEG.		
KW	Cellulose degradation; Hydrolyase; Glycosidase.		
FT	ACT_SITE 24		
FT	ACT_SITE 132 132		
FT	DISULEFID 4 16		
FT	DISULEFID 30 69		
FT	DISULEFID 32 176		
FT	DISULEFID 65 178		
FT	DISULEFID 72 157		
FT	DISULEFID 103 113		
SQ	SEQUENCE 181 AA; 19711 MW; E00A8C57203823P6 CRC64;		
Query Match	7.1%; Score 85; DB 1; Length 181;		
Best Local Similarity	32.5%; Pred. No. 0.867; Mismatches 37; Conservative 6; Indels 36; Gaps 9;		
QY	13 YGKDGSCQTG-----GACGYGNT-----YNGYGLYNAALSSALFND-----GAM 53		
Db	11 YNKGSCASTNYHDSHKACGCGPASGDAQPGWNA--GSFVAASQWYFPDCKKCMCGQ 68		
OY	54 CGACYTITCTCTSTQTKMCRG-----GNSITITATNLCXRNMAALPSNSGWCN 100		
Db	69 CGCGIKT-----TTGGYVPGGGPVREGSKTFMTTNC-PN-IYPMQD--WCN 114		

RN			"Nucleotide sequences of the envelope genes of two isolates of feline leukaemia virus subgroup B." ; <i>J. Virol.</i> 49:629-632(1984).
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=63216322; PubMed=6304347;		
RA	Elder J.H., Mullins J.I.;		
RT	"Nucleotide sequence of the envelope gene of Gardner-Arnstein feline leukemia virus B reveals unique sequence homologues with a murine mink cell focus-forming virus."		
RL	<i>J. Virol.</i> 46:871-880(1983).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84131936; PubMed=6321156.		
RA	Wunsch M., Schulz A.S., Koch W., Friedrich R., Hunsmann G.;		
RT	"Sequence analysis of Gardner-Arnstein feline leukaemia virus envelope gene reveals common structural properties of mammalian retroviral envelope genes."		
RL	EMBO J. 2:2239-2246(1983).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=88044502; Pubmed=2823466;		
RA	Gullhot S., Hampe A., D'Auriol L., Galibert F.;		
RT	"Nucleotide sequence analysis of the ITRs and env genes of SM-RSV and GA-FesV".		
RL	<i>Virology</i> 161:252-258(1987).		
CC	-I PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS. -----		
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DR	EMBL; K01209; AAAA3052.1; -.		
DR	EMBL; V01172; CAZ24497.1; -.		
DR	EMBL; X00188; CAA25008.1; -.		
DR	EMBL; M23026; -. NOT_ANNOTATED_CDS.		
PIR	A03991; VCVMGF.		
PIR	B33741; VCMWS2.		
HSSP	P03385; IMOF.		
DR	IInterPro: IPRO02050; Env_Polyprotein.		
DR	pfam: PF00429; ENV_polyprotein; 1.		
KW	Coot protein; Glycoprotein; Polyprotein; Signal.		
FY	SIGNAL 1 33 KNOR PROTEIN GP70. SPIKE PROTEIN PLSE. R PROTEIN.		
FT	CHAIN 34 465 645		
FT	CHAIN 466 645 662		
FT	CHAIN 646 662 662		
FT	CARBOHYD 43 43 . N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 58 58 . N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 286 286 . N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 322 322 . N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 327 327 . N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 351 351 . N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 354 354 . N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 394 394 . N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 410 410 . N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 430 430 . MISSING (IN REF. 4).		
FT	CONFLECT 15 15 T->> I (IN REF. 4).		
FT	CONFLECT 41 41 V -> V (IN REF. 4).		
FT	CONFLECT 47 47 LVTKRK -> VOITNTQ (IN REF. 4).		
FT	CONFLECT 51 56 EPPTWF -> YEPLHV (IN REF. 4).		
FT	CONFLECT 70 75 ITGTTMNSDEPRFG -> LVGSWEIVLDPNNVKHGR YSSK (IN REF. 4).		
FT	CONFLECT 80 95 DOPMRMQRMT -> KTDDRKKOQTYY (IN REF. 4). NRKO -> PSLGPKTH (IN REF. 4). P -> A (IN REF. 4). V -> A (IN REF. 4). TYTPRT -> AMMKPS (IN REF. 4). KGVIHQGYOCGGGWCGCYDKRAVHSSTGECCR ->		

Ft	CONFLICT	208	208		TGSSODTNSCEGK (IN REF. 4).
Ft	CONFLICT	215	215	S -> A (IN REF. 4).	
Ft	CONFLICT	223	223	S -> M (IN REF. 4).	
Ft	CONFLICT	223	223	S -> T (IN REF. 4).	
Ft	CONFLICT	232	232	S -> T (IN REF. 4).	
Ft	CONFLICT	238	238	M -> S (IN REF. 4).	
Ft	CONFLICT	264	300	IESVLTTHSHSGNGCTGTGLTVLNASIALSTPPVPAS ->	
Ft	SEQUENCE	662 AA:	73149 MM:	TGSVAVARQDPTNLSAPRSVAPTMGM (IN REF. 4).	
So				1482088BD547CFFA7 CRC64:	
Query Match					
Best Local Similarity 7.2%, Score 86.5; DB 1; Length 662;					
Matches 32; Conservative 15; Mismatches 46; Indels 65; Gaps 5;					
Oy	14	GCKDGSCIMGACAGCGNL	-----NAGYELLYNAALSSALFNDGAMGCAGCYT	59	
Db	126	GPODFCAWVCETTGTEIWRPRTSMDYTIVKKGYTOGIYC-----	SSGGWCPCPYD	178	
Oy	60	ITCDTSORAKWKCPGNSTTTATNLCXNMMLPSNGCMCPPLXHFDMS--OPAMENIA	117		
Db	179	KAWHSSTT-----	---GASEGRCPNPLILOFTQKRQRTSMDC-	212	
Oy	118	VYQAGIVEVNYKRVXPORGSGIRFAISGHDFEELVTVT	155		
Db	213	-----PKSWGRLRLRSGYDPDLALFSVS	234		
RESULT 12					
ID	ENV_FSVST	STANDARD;	PRT;	534 AA.	
AC	P03392;				
Dt	21-JUL-1986	(Rel. 01, Created)			
Dt	21-JUL-1986	(Rel. 01, Last sequence update)			
Dt	16-OCT-2001	(Rel. 40, Last annotation update)			
De	ENV polyprotein precursor (Coat polyprotein) [Contains: Knob protein				
De	GP0; Spike protein p15E] (Fragment).				
GN	ENV.				
OS	Feline sarcoma virus (strain Snyder-Theilen).				
OC	Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.				
Ox	NCBI_TaxID=11780;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=64115095; PubMed=6319767;				
RA	Nunberg J.H., Williams M.E., Innis M.A.;				
RT	"Nucleotide sequences of the envelope genes of two isolates of feline				
RT	leukemia virus subgroup B.";				
RL	J. Virol. 49:629-632(1984).				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; K01208; ? NOT_ANNOTATED_CDS.				
DR	PIR; A03992; VCWWSF.				
DR	HSPD; P03385; IMOF.				
DR	InterPro; IPR002050; Env_polyprotein.				
DR	Pfam; PF00429; Env_polyprotein; 1.				
Kw	Coat protein; Glycoprotein; Polyprotein; signal.				
Ft	SIGNAL	1	33		
Ft	CHAIN	34	465		KNOB PROTEIN GP70.
Ft	CHAIN	466	>534		SPIKE PROTEIN p15E.
Ft	CARBOHYD	43	43		N-LINKED (GLCNAC. . .) (POTENTIAL).
Ft	CARBOHYD	58	58		N-LINKED (GLCNAC. . .) (POTENTIAL).
Ft	CARBOHYD	286	286		N-LINKED (GLCNAC. . .) (POTENTIAL).
Ft	CARBOHYD	322	322		N-LINKED (GLCNAC. . .) (POTENTIAL).
Ft	CARBOHYD	327	327		N-LINKED (GLCNAC. . .) (POTENTIAL).
Ft	CARBOHYD	351	351		N-LINKED (GLCNAC. . .) (POTENTIAL).
Ft	CARBOHYD	354	354		N-LINKED (GLCNAC. . .) (POTENTIAL).

[illegible]

ID	FUNCTION	TRIPLE	STANDARD	PRT	242 AA
AC	P43317				
DT	01-NOV-1995	(Rel. 32, Created)			
DT	01-NOV-1995	(Rel. 32, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last annotation update)			
DE	Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)				
DE	(Cellulase V) (EG V).				
GN	EC15.				
OS	Trichoderma reesei (Hypocrea jecorina).				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Hypocreales; Hypocreaceae; Hypocrea.				
OX	NCBI_TaxID=51453;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-QM9414 / RUT C-30;				
RA	MEDLINE=95075308; Pubmed=7984103;				
RX	Saladino A., Henricas B., Hoffman A.-M., Teleman O., Penttilae M.;				
RT	"A novel, small endoglucanase gene, eg15, from Trichoderma reesei				
RT	isolated by expression in yeast";				
RL	Mol. Microbiol. 13:219-228(1994).				
CC	-I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic				
CC	linkages in cellulose.				
CC	-I- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL				
CC	HYDROLASES).				
CC	-I- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).				
CC					
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
DR	EMBL: Z33381; CAA83846.1; -.				
DR	HSSP: P00725; 2CEH.				
DR	InterPro: IPR000354; CBD_fungal.				
DR	InterPro: IPR000334; Glyco_hydro.45.				
DR	Pfam: PF00734; CBD.1; 1.				
DR	Pfam: PF02015; Glyco_hydro.45; 1.				
DR	Prodom: PD001821; CBD_fungal; 1.				
DR	SMART; SM00236; ICBD; 1.				
DR	PROSITE; PS00562; CBD_FUNGAL; 1.				
DR	PROSITE; PS00842; EXPANSIN_EG45; 1.				
DR	PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.				
KW	Cellulose degradation; Hydrolase; Glycosidase; signal.				
FT	SIGNAL	1	17		
FT	CHAIN	18	242		
FT	ACT_SITE	27	27		
FT	ACT_SITE	134	134		
FT	DOMAIN	18	182		
FT	DOMAIN	183	205		
FT	DOMAIN	206	242		
FT	CARBHYD	182	182		
FT	DISULFID	213	230		
FT	DISULFID	224	240		
FT	SEQUENCE	242 AA:	24411 MW;		
FT	SEQUENCE		CC033FC51326C71D CRC64;		
QY	Query Match	11.2%;	Score 134;	DB 1;	Length 242;
QY	Best Local Similarity	32.8%;	Pred. No. 5.2e-05;		
QY	Matches	42;	Conservative 16;	Mismatches 40;	Indels 30;
QY				Gaps	9;
DB	3	SVAAQFAAFYGGKDSCTMGACG-YGNLYNAGYLYNAAALSSALFND-----GAKGK	55		
DB	16	SAVKATRTTTRYDQDEGACGCGSSGCAFPWOLIGTNGVYTAAGSOALFDPAAGASWCAAGCG	75		
QY	56	ACTTICDPTQSOT--KMKKRPG---GNSITITATNLKCPNNALPNSGSGWCMNPPL-----	103		
DB	76	KCYQLT-STDQAPCCSGGTGGAAGOSTIIVWTLNC-PN-----NGNMQWC--PYVGGTNOY	127		
QY	104	---XHEDM	108		

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ID MP21_MAIZE STANDARD; PRT; 191 AA.
AC 007154;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Pollen allergen Zea m 1 (Zea m 1).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RX MEDLINE=94010312; PubMed=8406014;
RA Broadwater A.H., Rubinstein A.L., Chay C.H., Klapper D.G.,
RA Redinger P.A.;
RT "Zea m1, the maize homolog of the allergen-encoding Lol p1 gene of
RT rye grass."
RL Gene 131:227-230(1993).
CC -1- TISSUE SPECIFICITY: POLLEN TISSUE.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION LOW BEFORE AND HIGH AFTER
CC POLLEN MITOSIS.
CC -1- DISEASE: CAUSES MAIZE POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P 1 FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
CC -----
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CC -----
DR EMBL: L14271; AAA33496.1; -
DR PIR: JC1524; JC1524.
DR HSSP: P43214; IMHO.
DR MalzEDB: 65840; -
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSIN_FAMLY.
DR ProDom: PD002179; Pollen_allergen; 1.
DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen; multigene family.
FT DOMAIN 1 91 EXPANSIN-LIKE EG45.
FT DOMAIN 105 186 EXPANSIN-LIKE CBD.
SQ SEQUENCE 191 AA; 21362 MW; 6E2A9DF921C45C63 CRC64;

Query Match 13.2%; Score 157.5; DB 1; Length 191;
Best Local Similarity 27.7%; Pred. No. 3.4e-07;
Matches 53; Conservative 32; Mismatches 67; Indels 39; Gaps 11;

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ID MPCL_CYNDA STANDARD; PRT; 246 AA.
AC 004701;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Major pollen allergen Cyn d 1.
CN CYND1.
OS Cynodon dactylon (Bermuda grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Chloridoideae; Cyndontaeae; Cynodon.
OX NCBI_TaxID=28909;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=pollen;
RX MEDLINE=96347957; PubMed=8757211;
RA Smith P.M., Suphlioglu C., Griffith I.J., Theriault K., Knox R.B.,
RA Singh M.B.;
RT "Cloning and expression in yeast Pichia pastoris of a biologically
RT active form of Cyn d 1, the major allergen of Bermuda grass pollen."
RL J. Allergy Clin. Immunol. 98:331-343(1996).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P 1 FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: S83343; AAB50734.2; -
DR HSSP: P43214; IMHO.
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSIN_FAMLY.
DR ProDom: PD002179; Pollen_allergen; 1.
DR PROSITE: PS50843; EXPANSIN_CBD; 1.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KW Allergen.
FT DOMAIN 39 145 EXPANSIN-LIKE EG45.
FT DOMAIN 159 240 EXPANSIN-LIKE CBD.
FT CARBOHYD 9 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 246 AA; 26888 MW; 43DB8442DBA588322 CRC64;

Query Match 13.1%; Score 157; DB 1; Length 246;
Best Local Similarity 25.5%; Pred. No. 4.8e-07;
Matches 59; Conservative 38; Mismatches 96; Indels 38; Gaps 11;

```

RESULT 6

RESULT 7

RN SEQUENCE FROM N.A.
 RP TISSUE-Another:
 RX MEDLINE=9606591; PubMed=7590339;
 RA Xu H., Theetarakulpisut P., Goulding N., Suphioglu C., Singh M.B.,
 RA Balla P.L.;
 RT "Cloning, expression and immunological characterization of Ory s 1,
 RT the major allergen of rice pollen.";
 RL Gene 164:255-259(1995).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MATURE ANTHERS BUT NOT IN
 CC VEGETATIVE OR OTHER FLORAL TISSUES.
 CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
 CC -1- SIMILARITY: BELONGS TO THE LO1 P 1 FAMILY OF ALLERGENS.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 CC -----
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 CC -----
 DR EMBL; U31771; AAA86533.1; -;
 DR HSSP; P43214; IMHO.
 DR InterPro; IPR000882; Pollen_allergen.
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PRO1225; EXPANSINPFLY.
 DR PRODOM; PD00179; Pollen_allergen; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.
 KW Allergen; Glycoprotein; Signal; Multigene family.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 263 MAJOR POLLEN ALLEGEN ORY S 1.
 FT DOMAIN 61 164 EXPANSIN-LIKE EG45.
 FT DOMAIN 178 259 EXPANSIN-LIKE CBD.
 FT CARBOHYD 32 32 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 263 AA; 28497 MW; B1CF54E39BD60 CRC64;
 Query Match 13.7%; Score 163.5; DB 1; Length 263;
 Best Local Similarity 29.8%; Pred. No. 1.4e-07;
 Matches 53; Conservative 29; Mismatches 63; Indels 33; Gaps 9;
 QY 23 GGAGCYGNLYNAGCYGLYNALSSALFNDGAMCGACTTTCDTISQTRKWCXPGGNSITITAT 82
 DB 61 GGAGCYKRDVDRKAPFLGMSNCGNDPIFKDGCGSCFEIIC--SKEPACSDKDALHVTDM 118
 QY 83 NLICXNMALPNSGMCNPLX--HFDMSQPMW----ENIAYVOAGIVPVNKKRVPXQRS 136
 DB 119 N-----DEPIAAHYHFDLSGLMAMDGRKBEELRKAGIIDTQGRRVYCKTP 162
 QY 137 GG--IRFAL---SGHDYFELVTVTNVGSQVYAQMSI--KSGNTGMAMSRMGANMQ 187
 DB 163 ADTKTFPIHEKASNPNTYALT--VKYVAGDGVYVEVEIKEGSGEE--WKALKESGAIWR 218
 RESULT 4
 MPH1_HOLLA STANDARD: PRT; 265 AA.
 AC P43216; Q39975;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 01-MAR-2002 (Rel. 41, last annotation update)
 DE Major pollen allergen Hol 1 precursor (Hol 1 I) (Hol 1 1.0101 and
 DE 1.0102).
 OS Holcus lanatus (Velvet grass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 CC Poaceae; Holcus
 NC NCBI_TaxID=29679;
 RM [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN-CV. AVENEA: TISSUE=Pollen;
RA Schramm G.D., Bufe A., Becker W.M., Schlaak M.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE OF 18-265 FROM N.A.
RC STRAIN-CV. AVENEA: TISSUE=Pollen;
RA Schramm G.D., Bufe A., Petersen A., Haas H., Schlaak M., Becker W.M.;
RT "Mapping of IgE-binding epitopes on the recombinant major group I
  allergen of velvet grass pollen, rHol 1.1.";
RL J. Allergy Clin. Immunol. 99:781-787(1997).
RN
RP CHARACTERIZATION.
RC STRAIN-CV. AVENEA: TISSUE=Pollen;
RA MEDLINE=96319506; PubMed=8768803;
RT "Identification and characterization of the major allergens of velvet
  grass (Holcus lanatus), Hol 1.1 and Hol 1.5.";
RL Int. Arch. Allergy Immunol. 110:354-363(1996).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE LO1 P I FAMILY OF ALLEGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
CC
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  or send an email to license@isb-sib.ch)
CC -----
CC EMBL, Z27084; CAA81610.1; -.
DR EMBL, Z68893; CAA93121.1; -.
DR HSSP; P43214; IMHO.
DR InterPro; IPR000882; Pollen_allergen.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR ProDom; PD002179; Pollen_allergen; 1.
DR PROSITE; PS00843; EXPANSIN_CBD; 1.
DR PROSITE; PS00842; EXPANSIN_EG45; 1.
KW Allergen; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 265 MAJOR POLLEN ALLERGEN HOL 1.1.
FT DOMAIN 63 169 EXPANSIN-LIKE EG45.
FT DOMAIN 183 264 EXPANSIN-LIKE CBD.
FT VARIANT 103 103 T->S (IN HOL 1.1.0102).
SQ SEQUENCE 265 AA; 28590 MW; 1FE23B33EE198AD6D CRC64;
Query Match 13.3%; Score 159.5; DB 1; Length 265;
Best Local Similarity 26.2%; Pred. No. 3;le-07;
Matches 61; Conservative 39; Mismatches 90; Indels 43; Gaps 13;
OY 8 AFATVYGGKDGSCQM--GGACGYGMLYNAAGYLYNAAISSALFNDGAMGAGCYITTCDS 65
  I:::I: I: :|||||::: : I I I I I I: I
DB 46 AKSTWYGRPTGAPKPDNGGACGYKVDKPPFGMTGCGGTPHFKGGRGSGCFETKC-- 102
  66 QTKWKCKPGNSITITATNLCXNMALPSSGSGMCNPLX--HFDNSQAPMENA----- 117
  DB 103 -TKPESGCEPYTVHTD-----DN-----EPIPIYHFDLISGNAFGSMARKGERQ 147
  118 -VYQAGIYVNVKRPVXKRSQGR--FAI--SGHDYFELVTVTVNGSGVVAQMSIKGS 171
  DB 148 KLRASAGDELTKPRVRKCKYPDGTGKPFHVEKSSNPYITALL-VKYIDGQDVAVADIKER 206
  OY 172 NTG--WMAHSRNMGANMOSNA--YLAGQSISFTYO--LDDGRKRVTAANNAKPNM 219
  DB 207 GKDKWTEKESGCAVAVRVDTPDKLFG--PFTVRYTTEGGTGGEADVIPEGW 256

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RESULT 2	MPAL_PHAAO	MPAL_PHAAO	STANDARD:	PRT:	269 AA.
ID	MPAL_PHAAO	STANDARD:	PRT:	269 AA.	
AC	Q41260;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, last sequence update)				
DT	01-MAR-2002 (Rel. 41, last annotation update)				
DE	Major pollen allergen Phn a 1 precursor (Phn a 1).				
OS	Phalaris aquatica (Canary grass).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
OC	Poaceae; Phalaris				
OX	NCBI_TaxID=28479;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Pollen;				
RX	MEDLINE=96105569; PubMed=8564724;				
RA	Suppliglu C., Singh M.B.;				
RT	"Cloning, sequencing and expression in <i>Escherichia coli</i> of Phn a 1				
RT	and four isoforms of Phn a 5, the major allergens of canary grass				
TM	pollen.";				

Query Match	13.7%	Score 164.5;	DB 1;	Length 269;
Best Local Similarity	27.0%;	Pred. No. 1,1e-07;		
Matches	63;	Conservative	39;	Mismatches 88;
			Indels	43;
			Gaps	14;
QY	8	AFATFVGKKGSGCTM--GGACGCGNLYNACGGLYNALSLALENDGAMCGACGNYITGDTG	65	
		: :	: : : :	: : : :
Db	50	AKSTWAGKPTGACPBKDMGACGYKVDVKAAPFNGCNTGCGNPIPFIDGAGCCSFEFLKC--S	107	
QY	66	QTWCKRPGGNSITTTATNLCXPNNALPNSGCMCPPLX--HEDMSOPAMENTA-----	117	
		: : : :	: : : :	: : : :
Db	108	KPESC--SGEPLIVHTD-----DN-----EEPIAYHFHDLSGHAAGSMKKCKEE	151	
QY	118	LYVQAGIVPVNRYKVPKORSGGIR--FAI---SGHDFFELVTVYNNGSGSVVAKOMSTKGS	171	
		: : : : : :	: : : :	: : : :
Db	152	INVGAGELTELQFRRVRCYKYPDGTKPTFHYEKGSNPYLLALL--VKYVDGDDVAVDIKK	210	
QY	172	NTG--NMAAMSNRANMOSNA--YLAQGSLSFITY--LDGRKRTANNAAXXNW	219	
		: : : : : :	: : : :	: : : :
Db	211	GKDKWIELMESMAIKWIRIDPPDKLTG--PFYRYITTEGGTKAEFEEDVIFEGW	260	

Result 3			
MPOL_ID	MPOL_ORYSA	STANDARD:	PRT: 263 AA.
AC	Q40638;		
1-DT	01-NOV-1997 (Rel. 35, Created)		
2-DT	01-NOV-1997 (Rel. 35, Last sequence update)		
3-DT	01-MAR-2002 (Rel. 41, Last annotation update)		
4-DT	Major pollen allergen Ory s 1 precursor (Ory s I).		
5-DT	Oryza sativa (Rice)		
6-DT	Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;		
7-DT	Spemacotphyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
8-DT	Eumariolidae; Oryzeae; Oryza.		
9-DT	NCBI_TaxID=4550;		

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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:50:30 ; Search time 5.86347 Seconds
(without alignments)
1499.000 Million cell updates/sec

Title: US-09-896-301-4
Perfect score: 1197
Sequence: 1 KXSVAGSAFATFYGKDGSC.....KVTANXAPXNMLXXXXXX 227

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172.5	14.4	269	1 MP1L_LOLPR	P14946 lolium pere
2	164.5	13.7	269	1 MP1L_PHAPO	P41260 phalaris ag
3	163.5	13.7	263	1 MP0L_ORYSA	O40638 oryza sativ
4	159.5	13.3	265	1 MP2L_HOLIA	P42216 holcus lana
5	157.5	13.2	191	1 MP2L_MALIZ	Q07154 zea mays (m
6	157.5	13.1	246	1 MP0L_CYNDA	O04701 cynodon dac
7	152.5	12.7	263	1 MP0L_PHLPR	P43213 phleum prat
8	134	11.2	242	1 GUN5_TIRRE	P43317 trichoderma
9	91.5	7.6	668	1 ENY_FLV6	P21443 feline leuk
10	86.5	7.2	273	1 ENY_FLVCI	P21444 feline leuk
11	86.5	7.2	634	1 ENY_FSVGA	P03391 feline sarc
12	85.5	7.1	534	1 ENY_FSVST	P03392 feline sarc
13	85.5	7.1	662	1 ENY_FVLVB	P11261 feline leuk
14	85	7.1	181	1 GUN_MYTED	P82186 mytilus edu
15	84.5	7.1	432	1 ENV2_MOUSE	P11370 mus musculu
16	82.5	6.9	213	1 GUN5_HUMIN	P43316 humicola in
17	82	6.9	234	1 GLPF_THEMA	O9X163 thermotoga
18	82	6.9	436	1 ENY_FLVCS	Q02077 feline leuk
19	81.5	6.8	566	1 HEMA_IANJN	P03455 influenza a
20	81	6.7	595	1 SNX9_HUMAN	O9Y5X1 homo sapien
21	80.5	6.7	379	1 ADH2_SRPCA	P80468 struthio ca
22	80	6.7	662	1 PRCA_ANASP	O59149 anabaena sp
23	79	6.6	221	1 GP11_ZINOF	P82474 zingiber of
24	79	6.6	221	1 PGON_RAT	P53067 ratius norv
25	78.5	6.6	264	1 GLPF_STRCO	P19255 streptomyce
26	78.5	6.6	329	1 CYST_CAEEL	P25807 caenorhabdi
27	78.5	6.6	1385	1 YMS5_CAEEL	P34501 caenorhabdi
28	78	6.5	1268	1 PGON_MOUSE	P55066 mus musculu
29	77.5	6.5	433	1 SH06_ECOLI	P09750 escherichia
30	77.5	6.5	444	1 SH05_ECOLI	P09749 escherichia
31	77.5	6.5	444	1 SCAB_XENLA	P51169 xenopus lae
32	77.5	6.5	667	1 TSPE_BPP22	P12528 bacterioph
33	77.5	6.5	714	1 DL1L_RAT	P97677 ratius norv

34	77	6.4	348	1 PAP4_CARPA	P05994 carica papa
35	77	6.4	362	1 PCGY_CHICK	O90953 gallus gall
36	76.5	6.4	360	1 CYSE_HBMSP	P43156 hemerocalli
37	76	6.3	405	1 VGLG_HSVEA	P32650 equine herp
38	76	6.3	410	1 ENY_FLVCA	O02076 feline leuk
39	76	6.3	456	1 SHU7_ECOLI	P09751 escherichia
40	76	6.3	493	1 YBGH_ECOLI	P75742 escherichia
41	76	6.3	442	1 ENY_FLVGL	P08359 feline leuk
42	76	6.3	1045	1 GUNB_CRLFI	P26325 cellulomona
43	76	6.3	1822	1 ITB4_HUMAN	P16144 homo sapien
44	75.5	6.3	82	1 KRHA_SHEEP	O02958 ovis aries
45	75.5	6.3	573	1 ALP1_YEAST	P38971 saccharomyc

ALIGNMENTS

RESULT 1

ID	MP1L_LOLPR	STANDARD:	PRT:	263 AA.
AC	P14946: P19964:			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Pollen allergen lol p 1 precursor (lol p I) (Allergen R7).			
OS	Lolium perenne (Perennial ryegrass).			
OC	Eukaryota: Viridiplantae: Embryophyta: Tracheophyta;			
OC	Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; Pooidae;			
OC	Poaceae; Lolium.			
OX	NCBI_TaxID=4522:			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90375479; PubMed=1697854;			
RA	Perez M., Ishioka G.Y., Walker L.E., Chesnut R.W.;			
RT	"cDNA cloning and immunological characterization of the rye grass			
RT	allergen lol p I.";			
RL	J. Biol. Chem. 265:16210-16215(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 24-48.			
RC	TISSUE=Pollen;			
RX	MEDLINE=91160716; PubMed=2001733;			
RA	Griffith I.J., Smith P.M., Pollock J., Theerakulpisut P.;			
RT	Avoglia A., Davies S., Hough T., Singh M.B., Simpson R.J., Ward I.D.;			
RT	Knock R.B.;			
RT	"Cloning and sequencing of lol pI, the major allergenic protein of			
RT	rye grass pollen.";			
RT	FEBS Lett. 279:210-215(1991).			
RN	[3]			
RP	SEQUENCE OF 24-53.			
RC	TISSUE=Pollen;			
RX	MEDLINE=86242068; PubMed=3718469;			
RA	Cottam G.P., Moran D.M., Strandberg R.;			
RT	"Physicochemical and immunochemical characterization of allergenic			
RT	proteins from rye-grass (Lolium perenne) pollen prepared by a rapid			
RT	and efficient purification method.";			
RL	Biochem. J. 234:305-310(1986).			
RN	[4]			
RP	SEQUENCE OF 236-263.			
RX	MEDLINE=89364850; PubMed=2475768;			
RA	Esch R.E., Klapper D.G.;			
RT	"Isolation and characterization of a major cross-reactive grass group			
RT	I allergenic determinant.";			
RT	Mol. Immunol. 26:557-561(1989).			
RL	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- DISEASE: CAUSES GRASS POLLEN ALLERGY.			
CC	-1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.			
CC	-1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE E645 DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE EXPANSIN 2.
 GN EXP2.
 OS Prunus avium (Cherry).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
 OC Eucosids 1: Rosales: Rosaceae: Amygdaloideae: Prunus.
 OC NCBI_TaxID=42229;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu Z., Miersma P.A.;
 RT "Differential Expression of Expansin Genes Isolated from Sweet Cherry
 (Prunus avium L.) During Fruit Ripening."
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF297522; AAC13983.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen.1.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 252 AA; 26766 MW; 5C62EBF83E5A138E CRC64;

Query Match 63.5%; Score 760.5; DB 10; Length 252;
 Best Local Similarity 64.6%; Pred. No. 2, 8e-62;
 Matches 137; Conservative 25; Mismatches 47; Indels 3; Gaps 2;

OY 8 AFATFYGKDGSCITMGACGYGNLYNAGYGLYNALSSALFNDGAMGACYYTTCDSQT 67
 ID 09FY31 PRELIMINARY; PRT; 253 AA.
 AC 09FY31;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE EXPANSIN.
 GN EXP1.
 OS Festuca pratensis.
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Poideae:
 OC Poaceae: Festuca.
 OC NCBI_TaxID=4608;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV. PREFEST; TISSUE=ROOT;
 RC MEDLINE=21377433; PubMed=11485205;
 RA Reidy B., McQueen-Mason S., Noesberger J., Fleming A.;
 RT "Differential Expression of alpha- and beta-expansin genes in the
 elongating leaf of Festuca pratensis."
 RL Plant Mol. Biol. 46:491-504(2001).
 DR EMBL: AJ276006; CAC06432.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 253 AA; 26547 MW; BEB18079F6400A89 CRC64;

RESULT 14
 OYFY31
 ID 09FY31 PRELIMINARY; PRT; 253 AA.
 AC 09FY31;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE EXPANSIN.
 GN EXP1.
 OS Festuca pratensis.
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Poideae:
 OC Poaceae: Festuca.
 OC NCBI_TaxID=4608;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV. PREFEST; TISSUE=ROOT;
 RC MEDLINE=21377433; PubMed=11485205;
 RA Reidy B., McQueen-Mason S., Noesberger J., Fleming A.;
 RT "Differential Expression of alpha- and beta-expansin genes in the
 elongating leaf of Festuca pratensis."
 RL Plant Mol. Biol. 46:491-504(2001).
 DR EMBL: AJ276006; CAC06432.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 253 AA; 26547 MW; BEB18079F6400A89 CRC64;

Query Match 63.5%; Score 759.5; DB 10; Length 253;
 Best Local Similarity 63.3%; Pred. No. 3, 5e-62;
 Matches 133; Conservative 31; Mismatches 45; Indels 1; Gaps 1;

OY 10 AFYGGKDGSCITMGACGYGNLYNAGYGLYNALSSALFNDGAMGACYYTTCDSQTFK 69
 ID 09FY30 PRELIMINARY; PRT; 252 AA.
 AC 09FY30;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE EXPANSIN.
 GN EXP2.
 OS Festuca pratensis.
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Poideae:
 OC Poaceae: Festuca.
 OC NCBI_TaxID=4608;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV. PREFEST; TISSUE=LEAF ELONGATION ZONE;
 RC MEDLINE=21377433; PubMed=11485205;
 RA Reidy B., McQueen-Mason S., Noesberger J., Fleming A.;
 RT "Differential Expression of alpha- and beta-expansin genes in the
 elongating leaf of Festuca pratensis."
 RL Plant Mol. Biol. 46:491-504(2001).
 DR EMBL: AJ276007; CAC06433.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 252 AA; 26544 MW; BEB624E919F42238 CRC64;

Query Match 63.4%; Score 759; DB 10; Length 252;
 Best Local Similarity 65.0%; Pred. No. 3, 9e-62;
 Matches 139; Conservative 24; Mismatches 49; Indels 2; Gaps 1;
 OY 6 OSATFYGKDGSCITMGACGYGNLYNAGYGLYNALSSALFNDGAMGACYYTTCDS 65
 ID 09FY30 PRELIMINARY; PRT; 252 AA.
 AC 09FY30;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE EXPANSIN.
 GN EXP2.
 OS Festuca pratensis.
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Poideae:
 OC Poaceae: Festuca.
 OC NCBI_TaxID=4608;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV. PREFEST; TISSUE=LEAF ELONGATION ZONE;
 RC MEDLINE=21377433; PubMed=11485205;
 RA Reidy B., McQueen-Mason S., Noesberger J., Fleming A.;
 RT "Differential Expression of alpha- and beta-expansin genes in the
 elongating leaf of Festuca pratensis."
 RL Plant Mol. Biol. 46:491-504(2001).
 DR EMBL: AJ276007; CAC06433.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 252 AA; 26544 MW; BEB624E919F42238 CRC64;

Query Match 63.4%; Score 759; DB 10; Length 252;
 Best Local Similarity 65.0%; Pred. No. 3, 9e-62;
 Matches 139; Conservative 24; Mismatches 49; Indels 2; Gaps 1;
 OY 6 OSATFYGKDGSCITMGACGYGNLYNAGYGLYNALSSALFNDGAMGACYYTTCDS 65
 ID 09FY30 PRELIMINARY; PRT; 252 AA.
 AC 09FY30;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE EXPANSIN.
 GN EXP2.
 OS Festuca pratensis.
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Poideae:
 OC Poaceae: Festuca.
 OC NCBI_TaxID=4608;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV. PREFEST; TISSUE=LEAF ELONGATION ZONE;
 RC MEDLINE=21377433; PubMed=11485205;
 RA Reidy B., McQueen-Mason S., Noesberger J., Fleming A.;
 RT "Differential Expression of alpha- and beta-expansin genes in the
 elongating leaf of Festuca pratensis."
 RL Plant Mol. Biol. 46:491-504(2001).
 DR EMBL: AJ276007; CAC06433.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 252 AA; 26544 MW; BEB624E919F42238 CRC64;

Search completed: October 11, 2002, 14:59:41
 Job time: 20.6007 secs

RL Curr: Opin. Plant Biol. 4:527-532(2001).
DR EMBL: AF394544; AAL24480.1; -
SQ SEQUENCE 251 AA; 26674 MW; C450366570EFE3BD CRC64;

Query Match	64.4%	Score 770.5;	DB 10;	Length 251;
Best Local Similarity	65.4%;	Pred. No. 3.4e-63;		
Matches 140;	Conservative 24;	Mismatches 47;	Indels 3;	Gaps 2;

[illegible]

RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AC007789; AAD38297.1; -
 DR EMBL: AP002865; BAB18338.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMILY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 DR SEQUENCE 254 AA; 26987 MW; AA0924E21A819101 CRC64;

Query Match 67.6%; Score 809.5; DB 10; Length 254;
 Best Local Similarity 67.6%; Pred. No. 8.9e-67;
 Matches 144; Conservative 22; Mismatches 46; Indels 1; Gaps 1;

OY 7 SAFATFYGGKDSCTMGACGCGYGNLYNAGYGLYNALSSALFENDGAMGACACTTTCDSQ 66
 DB 29 SATATFYGGSDASGTMGSCGCGNNISAGYGTNTTALSSALYGDASGACACTVTCDA 88
 OY 67 TKWCKPFGNSITTTATNLCPNMALPNSGWCNPELXHFDM SOPAMENIAYGAGIYPV 126
 DB 89 TKWCK-NGTSYVVTATNYCPRNYSBGDAGWCNPRRHFDMSOPAMEAIAYSSGIYPV 147
 OY 127 NKRRPXRSGIRRAISGHDFELYVTYNNVGGSGVVAQMSIKSNTGMMAMSRNMGANW 186
 DB 148 RARPCRRVGGIRFGIAGHDYELVLTYNVAGVAAVAWKGSGTEWLSMRNMGANW 207
 OY 187 QSNATLAGOSLSEFYQLDDGKRYTAMNXPXNW 219
 DB 208 QSNATLTGQALSFYQADGCVTAIVDAVPANW 240

RESULT 5
 Q39625 PRELIMINARY; PRT; 250 AA.

ID 039625; AC 039625; DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE EXPANSIN SL.
 GN CS-EXP1.
 OS Cucumis sativus (Cucumber).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 OX NCBI_TaxID=3659;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BURPEE PICKLER;
 RX MEDLINE=96016146; PubMed=7568110;
 RA Sheehan T.Y., Shi Y., Durachko D.M., Gullinan M.J.,
 RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
 RT "Molecular cloning and sequence analysis of expansins--a highly
 RT conserved, multigene family of proteins that mediate cell wall
 RT extension in plants.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
 DR EMBL: U30382; AAB37746.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMILY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 FT CHAIN 24 250
 SQ SEQUENCE 250 AA; 27215 MW; 60651BC47E4186DA CRC64;

Query Match 64.6%; Score 773.5; DB 10; Length 250;
 Best Local Similarity 64.5%; Pred. No. 1.8e-63;
 Matches 138; Conservative 27; Mismatches 46; Indels 3; Gaps 2;

OY 6 QSAFATFYGGKDSCTMGACGCGYGNLYNAGYGLYNALSSALFENDGAMGACACTTTCDS 65
 DB 29 QSGHATFYGGSDASGTMGACGCGYGNLYSOGYGTNTTALSTALFNNGLSGACACEMTC-IN 87
 OY 66 OTWKCKPFGNSITTTATNLCPNMALPNSGWCNPELXHFDM SOPAMENIAYGAGIYPV 125
 DB 88 DPAWKCPG-TIRVATINFCPPNFALPNNNGWCNPPLOHFDMAEPALFOIAQYRAGIYV 145

OY 126 VVKRXPXORSGGIRFAISGHDFELYVTYNNVGGSGVVAQMSIKSNTGMMAMSRNMGAN 185
 DB 146 VSFRVPCMKKGVAFITNGHSYFNVLITVNGCAGDVHSVSTIGSRIGWQSMRNGON 205
 OY 186 WQSNATLAGOSLSEFYQLDDGKRYTAMNXPXNW 219
 DB 206 WQSNATLTGQALSFYQVLTSDGRITLAVNLVPSNW 239

RESULT 6
 Q94619 PRELIMINARY; PRT; 250 AA.

ID 094619; AC 094619; DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ALPHA-EXPANSIN.
 GN EXP12.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzaeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21521099; PubMed=11641069;
 RA Lee Y., Choi D., Kende H.;
 RT "Expansins: ever-expanding numbers and functions.";
 RL Curr. Opin. Plant Biol. 4:527-532(2001).
 DR EMBL: AF394548; AL24484.1; -
 SQ SEQUENCE 250 AA; 26429 MW; AEE0729BAF81079B CRC64;

Query Match 63.1%; Score 772.5; DB 10; Length 250;
 Best Local Similarity 63.1%; Pred. No. 2.2e-63;
 Matches 137; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

OY 3 SVASAFATFYGGKDSCTMGACGCGYGNLYNAGYGLYNALSSALFENDGAMGACACTTTC 62
 DB 22 AALSGTATFYGGSDASGTMGACGCGYGNLYSTGYTNTALSSALFENDGACGCEYQITC 81
 OY 63 DTGOTWKCKRKGNSITTTATNLCPNMALPNSGWCNPELXHFDM SOPAMENIAYGAG 122
 DB 82 DQNSKWKCK-AGTSVITTTATNLCPDYSKPSNDGWCNPPROHFDMAQPAWQIGYRGG 140
 OY 123 IYDVNPKRXPXORSGGIRFAISGHDFELYVTYNNVGGSGVVAQMSIKSNTGMMAMSRN 182
 DB 141 IYDVNFORVSCTRKGGVRFITNGNSYFELVLTINVGPGSISVQIKTKTKGTWTSRW 200
 OY 183 GAWQSNATLAGOSLSEFYQLDDGKRYTAMNXPXNW 219
 DB 201 GAWQSNATLTGQALSFYQVLTSDGRITLAVNLVPSNW 237

RESULT 7
 Q94611

ID 094611; AC 094611; PRELIMINARY; PRT; 251 AA.

DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ALPHA-EXPANSIN.
 GN EXP2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzaeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21521099; PubMed=11641069;
 RA Lee Y., Choi D., Kende H.;
 RT "Expansins: ever-expanding numbers and functions.";

QY 61 TCOTSTQKCKPGNSGCGTTCATATNLCXPNMALPSNSGCGCNPPLXHDMSOPAMENTAVYQ 120
 DB 84 TCDTSQTKCKPGNSGCGTTCATATNLCXPNMALPSNSGCGCNPPLQHDMSOPAMENTAVYQ 143
 QY 121 AGIVPVYKRVKXQKSGIRFPAISGHDYFELVYTVTVNGSGGVAOMSIKSNMGMAKMSR 180
 DB 144 AGIVPVYKRVKXQKSGIRFPAISGHDYFELVYTVTVNGSGGVAOMSIKSNMGMAKMSR 203
 QY 181 MGNAMQSNAYLAGQSLSFVQLDDGGRKVTAMNXPXNM 219
 DB 204 MGNAMQSNAYLAGQSLSFVQLDDGGRKVTAMNXPXNM 242

RESULT 2
 Q9XHX0 PRELIMINARY: PRT: 251 AA.
 ID Q9XHX0
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PUTATIVE EXPANSIN.
 GN T49B20.23 OR P0034C11.27.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzaeae; Oryza.
 NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Buell C.R., Benito M.-I., Lin X., Mason T.M., Umayam L., Shea T.P.,
 RA Fujii C.Y., Shen M., Fraser C.M.;
 RT "Oryza sativa BAC T49B20 genomic sequence."
 DL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone:P0034C11."
 DL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC007789; ABD38296.1; -
 DR EMBL: AP002865; BAB1836.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen.1.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR ProDom: PD002179; Pollen_allergen.1.
 DL PRODOM: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 251 AA; 26334 MW; 1A0BB36709FDF9A3 CRC64;

Query Match 74.0%; Score 885.5; DB 10; Length 251;
 Best Local Similarity 76.4%; Pred. No. 8.8e-74;
 Matches 162; Conservative 15; Mismatches 34; Indels 1; Gaps 1;
 QY 8 AFATFYGGKDGSGCTMGACGCGNLYNAGYGLYNALSSALFNDGAMCGACTTTCDSOT 67
 DB 28 AFATFYGGSGASGCTMGACGCGDLYGAGYCTRTAALSTALFNGAGCGACTTACCTRT 87
 QY 68 KWCKPGNSGTTTATNLCXPNMALPSNSGCGCNPPLXHDMSOPAMENTAVYQAGIVPVN 127
 DB 88 QMCKP-GTSTITATNLCXPNMALPSNSGCGCNPPLXHDMSOPAMENTAVYQAGIVPVN 146
 QY 128 YKRVKXQKSGIRFPAISGHDYFELVYTVTVNGSGGVAOMSIKSNMGMAKMSR 187
 DB 147 YKRVKXQKSGIRFPAISGHDYFELVYTVTVNGSGGVAOMSIKSNMGMAKMSR 206
 QY 188 SNAAYLAGQSLSFVQLDDGGRKVTAMNXPXNM 219
 DB 207 SNAAYLAGQSLSFVQLDDGGRKVTAMNXPXNM 238

RESULT 3
 Q9FY29 PRELIMINARY: PRT: 255 AA.
 ID Q9FY29

AC Q9FY29;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE EXPANSIN.
 GN EXP3.
 OS Festuca pratensis.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Poaceae; Festuca.
 NCBI_TaxID=4608;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. PREEST; TISSUE=ROOT;
 RX MEDLINE=2137433; PubMed=11485205;
 RA Reidy B., McQueen-Mason S., Noesberger J., Fleming A.;
 RT "Differential Expression of alpha- and beta-expansin genes in the
 RL elongating leaf of Festuca pratensis."
 DR EMBL: AJ276008; CAC06434.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PR01225; EXPANSINFAMLY.
 DR ProDom: PD002179; Pollen_allergen.1.
 DL PRODOM: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 255 AA; 27358 MW; 5B1082946042B3DC CRC64;

Query Match 72.4%; Score 866.5; DB 10; Length 255;
 Best Local Similarity 74.6%; Pred. No. 5e-72;
 Matches 159; Conservative 18; Mismatches 35; Indels 1; Gaps 1;
 QY 7 SAFATFYGGKDGSGCTMGACGCGNLYNAGYGLYNALSSALFNDGAMCGACTTTCDSO 66
 DB 31 SAFATFYGGKDGSGCTMGACGCGNLYNAGYGLYNALSPVLFNDGAMCGACTTTCDSO 90
 QY 67 KWCKPGNSGTTTATNLCXPNMALPSNSGCGCNPPLXHDMSOPAMENTAVYQAGIVPV 126
 DB 91 SMCN-AGKSTITSATNLCXPNMALPSNSGCGCNPPLXHDMSOPAMENTAVYQAGIVPV 149
 QY 127 NKRVKXQKSGIRFPAISGHDYFELVYTVTVNGSGGVAOMSIKSNMGMAKMSR 186
 DB 150 NKRVKXQKSGIRFPAISGHDYFELVYTVTVNGSGGVAOMSIKSNMGMAKMSR 209
 QY 187 QSNAYLAGQSLSFVQLDDGGRKVTAMNXPXNM 219
 DB 210 QSNAYLAGQSLSFVQLDDGGRKVTAMNXPXNM 242

RESULT 4
 Q9XHW9 PRELIMINARY: PRT: 254 AA.
 ID Q9XHW9
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PUTATIVE EXPANSIN.
 GN T49B20.24 OR P0034C11.29.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzaeae; Oryza.
 NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Buell C.R., Benito M.-I., Lin X., Mason T.M., Umayam L., Shea T.P.,
 RA Fujii C.Y., Shen M., Fraser C.M.;
 RT "Oryza sativa BAC T49B20 genomic sequence."
 DL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone:P0034C11."
 DL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:51:00 ; Search time 19.6007 Seconds
(Without alignments)
2003.488 Million cell updates/sec

Title: US-09-896-301-4

Perfect score: 1197

Sequence: 1 KXSVASQAFATFYGGKDGSC.....KVTAMNAPXNWLXXXXXX 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: sp._archaea:*
2: sp._bacteria:*
3: sp._fungi:*
4: sp._human:*
5: sp._invertebrate:*
6: sp._mammal:*
7: sp._mhc:*
8: sp._organelle:*
9: sp._phage:*
10: sp._plant:*
11: sp._rodent:*
12: sp._virus:*
13: sp._vertebrate:*
14: sp._unclassified:*
15: sp._virus:*
16: sp._bacteriap:*
17: sp._archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1173	98.0	255	10	Q40637 oryza sativ
2	885.5	74.0	251	10	Q9XHX0 oryza sativ
3	866.5	72.4	255	10	Q9FY29 festuca pra
4	809.5	67.6	254	10	Q9XHW9 oryza sativ
5	773.5	64.6	250	10	Q39625 cucumis sat
6	772.5	64.5	250	10	Q94619 oryza sativ
7	770.5	64.4	251	10	Q946J1 oryza sativ
8	769	64.2	256	10	Q92P39 oryza sativ
9	767	64.1	252	10	Q94K75 zea mays (m
10	765	63.9	257	10	Q9FVH0 lycopersico
11	764.5	63.9	252	10	Q9JNU3 arabidopsis
12	762.5	63.7	251	10	Q40636 oryza sativ
13	760.5	63.5	252	10	Q9FUM2 prunus aviu
14	759.5	63.5	253	10	Q9FY31 festuca pra
15	759	63.4	252	10	Q9FY30 festuca pra
16	757.5	63.3	247	10	Q82625 lycopersico

17	756	63.2	261	10	Q24208 oryza sativ
18	755.5	63.1	260	10	Q9FMT0 cicer ariet
19	751	62.7	256	10	Q9ZP38 nicotiana t
20	750.5	62.7	232	10	Q93493 pinus taeda
21	750.5	62.7	232	10	Q93495 pinus taeda
22	750.5	62.7	253	10	Q9SWY1 pinus taeda
23	750	62.7	257	10	Q9ZP37 nicotiana t
24	747.5	62.4	252	10	Q93492 pinus taeda
25	747.5	62.4	254	10	Q82093 prunus arme
26	746.5	62.4	254	10	Q9FUM3 prunus aviu
27	746.5	62.4	257	10	Q9XG16 lycopersico
28	746.5	62.4	260	10	Q9M2S9 arabidopsis
29	744.5	62.2	247	10	Q9M517 tribhysaria
30	744.5	62.2	249	10	Q9LDR9 arabidopsis
31	743.5	62.1	246	10	Q93442 oryza sativ
32	743.5	62.1	249	10	Q9ZP35 nicotiana t
33	743.5	62.1	250	10	Q9FVG9 oryza sativ
34	742.5	62.0	246	10	Q946J0 oryza sativ
35	742.5	62.0	264	10	Q9MAX6 oryza sativ
36	742.5	62.0	267	10	Q946H9 oryza sativ
37	740.5	61.9	245	10	Q9LBB2 zinnia eleg
38	740.5	61.9	253	10	Q94KT7 zea mays (m
39	740	61.8	257	10	Q9FYS7 striga asia
40	738.5	61.7	249	10	Q9M515 tribhysaria
41	738.5	61.7	260	10	Q81999 lycopersico
42	737.5	61.6	232	10	Q93494 pinus taeda
43	736.5	61.5	253	10	Q93XP2 prunus cera
44	736.5	61.5	258	10	Q39626 cucumis sat
45	736.5	61.5	262	10	Q946I7 oryza sativ

ALIGNMENTS

RESULT 1

ID Q40637 PRELIMINARY: PRT: 255 AA.
AC Q40637:
BT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EXPANSIN OS-EXP3.
GN OS-EXP3.
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPONBARE;
RX MEDLINE=96016146; PubMed=7568110;
RA Shcherban T.Y., Shi J., Durachko D.M., Gultinan M.J.,
RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansins--a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RT Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RL EMBL: U30479; AAB38075.1; -;
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSINFAMILY.
DR PRODOM: PD002179; Pollen_allergen; 1.
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Query Match

Best Local Similarity 98.0%; Score 1173; DB 10; Length 255;
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QY 1 KXSVASQAFATFYGGKDGSCCTMGACGTCGNLYNAGYGLYNAALSSALFNDCAMGCACYTI 60
DB 24 KXSVASQAFATFYGGKDGSCCTMGACGTCGNLYNAGYGLYNAALSSALFNDCAMGCACYTI 83

PR 22-OCT-1999; 99US-0160989.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match

Best Local Similarity 77.0%; Score 927.5; DB 21; Length 259;
Matches 167; Conservative 22; Mismatches 29; Indels 9; Gaps 2;

OY 3 GPMINAHATPEYXXGDAAXXTGACGAGCNLYSOGYGLFTALSTALPLDGLSCGACXELMC 62
DB 34 GGMINAHATPEYXXGDAAXXTGACGAGCNLYSOGYGLFTALSTALPLDGLSCGACXELMC 62
OY 63 VNDPQICIGRSTIVTATNFCPP-----GGACDPNHHFDLSQPIYKIALYKSGIT 114
DB 94 ENDGKMCCLPG-SIVVTATNFCPPNNALANNNGCMCPLEHFDLQAPVQRIAYRAGIV 152
OY 115 PVYRVRCKRSGIRFTINGHSYFVLVTNNGAGDVHSVMKSGRTKQWLSRNMGO 174
DB 153 PVYRVRCKRSGIRFTINGHSYFVLVTNNGAGDVHSVMKSGRTKQWLSRNMGO 212
OY 175 NMOSNYLNGQSLSFVYVTSDBRSVVSFVNAPPTWSFGQTYTGQFR 221
DB 213 NMOSNYLNGQSLSFVYVTSDBRSVVSFVNAPPTWSFGQTYTGQFR 259

RESULT 15

AGS1631
ID AGS1631 standard; Protein: 259 AA.

XX AGS1631;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 65549.

KM Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

XX Arabidopsis thaliana.

OS EPI033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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Best Local Similarity 73.6%; Pred. No. 7.8e-95;
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DB 24 GCMINAHATFYGGDASGTWGGACGCGNLYSGGXTETALSTALPDGSCCACKELMC 83
QY 63 VNDPQWCIKRSIVTATNCP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
DB 84 ENDGKWCLPG-SIVVTATNFCPPNNMLANNNGCMCNPLEHFDLAPVFORIAQYRAGIV 142
QY 115 PVWYRRYRCKRSGGIRPTINGHSYFNLVLTNNGAGDVHSVSMKSRKQWLSRNMQO 174
DB 143 PVSTRYRCPKRRGCIREFTLNGHSYFNLVLTNNGAGDVHSAIKSRVWQAMSRNQO 202
QY 175 NMQSNSTYLNQSLSFVYTTSDRSRVVSFNVAPPTMSFGQTYTGQPR 221
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DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3355.
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KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
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PN EP103405-A2.
XX
PD 06-SEP-2000.
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PE 25-FEB-2000; 2000EP-0301439.
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PR 05-MAR-1999; 99US-0123180.
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PR 08-APR-1999; 99US-0128714.
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Query Match 77.0%; Score 927.5; DB 21; Length 249;
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RESULT 12
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 DT 18-OCT-2000 (first entry)
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 KW Protein identification; signal transduction pathway; metabolic pathway;
 hybridisation assay; genetic mapping; gene expression control; promoter;
 termination sequence.
 KW
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
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 XX 25-FEB-2000; 2000EP-0301439.
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XX AAG06545;
AC AAG06545;
DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 3356.
DE
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
PN EPI033405-A2.
XX EPI033405-A2.
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PE 25-FEB-2000; 2000EP-0301439.
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AAGS1647;

18-OCT-2000 (first entry)

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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PE 25-FEB-2000; 2000EP-0301439.

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XX 18-OCT-2000 (first entry)

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QY 142 VLVTVNGAGDVHSVSKSGRTKQMLSRMNGWQNSNLTNGOSLSFVVTTSIDRSYVS 201
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RESULT 8
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AC 17-OCT-2000 (first entry)
DT
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XX Protein identification: signal transduction pathway; metabolic pathway;
KW hydralisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 64704.
DE Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX EPI033405-A2.
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QY	82	FCPPGAGACDPENHHFDSLQPIYERIKALYKSGIIPVMRRVRCRKSRSIGREPTINGHSYENL	141
Db	61	FCPPGAGACDPENHHFDSLQPIYERIKALYKSGIIPVMRRVRCRKSRSIGREPTINGHSYENL	120
QY	142	VLVTNVGAGAGDVHSVSKMGSFTKQOLMSRNMGQWQNSNLYNGQSLSFVVTSDRSRVS	201
Db	121	VLVTNVGAGAGDVHSVSKMGSFTKQOLMSRNMGQWQNSNLYNGQSLSFVVTSDRSRVS	180
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AC	AA651014;
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DT	18-OCT-2000 (first entry)

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Query Match 98.6% Score 1187; DB 21; Length 221;
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DB 121 RCKRSGIRFTINGHSYFNLVLTWVGAGDVHSVSKSGRTKQWQMSRMGQNMOSNSY 180
QY 182 LNCOSLSFVVTSDRSVSVFNAPPMWSCGYTGTGQFFRY 222
DB 181 LNCOSLSFVVTSDRSVSVFNAPPMWSCGYTGTGQFFRY 221
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RESULT 6
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ID AAG15695 standard; Protein: 201 AA.
XX AAG15695:
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DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16049.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;

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KW termination sequence.
XX
OS Arabidopsis thaliana.
XX EPI033405-42.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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QY 62 CVNDPQMCIKGRSIVVTATNFCPPGACDPPNHHFDLSQPIYEKIALYKSGIIPWYRRV 121
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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PN EP1033405-A2.

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XX 04-APR-1996.
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XX 12-MAY-1994; 94AU-0066320.
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XX 12-MAY-1993; 93US-0060944.
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XX (PENN-) PENN STATE RES FOUND.
PI
XX Cosgrove DJ, McQueen-Mason S;
DR
XX WPI; 1996-201150/21.
XX
XX Expansin proteins which alter the mechanical strength of
PT poly:saccharide(s) - useful in paper mfr. and recycling
XX
XX Disclosure; Page 31; 60pp; English.
XX
XX Expansins are a novel class of proteins that catalyze the extension
CC of plant cell walls and the weakening of the hydrogen bonds in pure
CC cellulose. 2 Expansins (AAR94528 and AAR94529) have been identified in
CC rice and 3 in Arabidopsis (AAR94530-32). A cDNA clone (AAT13320)
CC coding for cucumber expansin 29 (AAR94527) has been obt'd. Expansins
CC can be used e.g. in the mfr. de-lignification and recycling of paper, in
CC the textile industry, to aid delignification processes, to alter gel
CC mechanical strength, etc.
XX
XX Sequence 222 AA:
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RESULT 4
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DT 17-OCT-2000 (first entry)
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
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PN EPI033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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XX 18-OCT-2000 (first entry)

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XX Protein identification; signal transduction pathway; metabolic pathway;

KM hybridisation assay; genetic mapping; gene expression control; promoter;

KM termination sequence.

OS Arabidopsis thaliana.

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XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	1187	98.6	221	21	AA651013 Arabidopsis thalia
6	1096	91.0	201	21	AA615695 Arabidopsis thalia
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XX	KW	hybridisation assay; genetic mapping; gene expression control; promoter;
XX	KW	termination sequence.
XX	OS	Arabidopsis thaliana.
XX	PN	EP1033405-A2.
XX	PD	06-SEP-2000.
XX	PF	25-FEB-2000; 2000EP-0301439.
XX	PR	25-FEB-1999; 99US-0121825.
XX	PR	05-MAR-1999; 99US-0123180.
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; LENGTH: 179
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US-09-362-642-6

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RESULT 13

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; APPLICANT: Cosgrove, Daniel J
; APPLICANT: McQueen-Mason, Simon
; APPLICANT: Gullitman, Mark J
; APPLICANT: Shcherban, Tatyana
; APPLICANT: Shi, Jun
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; FILE REFERENCE: 1194/JC114US3
; CURRENT APPLICATION NUMBER: US/09/092.160C
; CURRENT FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 08/440.517
; EARLIER FILING DATE: 1995-05-12
; EARLIER APPLICATION NUMBER: 08/242.090
; EARLIER FILING DATE: 1994-05-12
; EARLIER APPLICATION NUMBER: 08/060.944
; NUMBER OF SEQ ID NOS: 7
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; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
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      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      66 POWCIRK-GRSIVVATNFCPP-----GGACDPNNHFDLSQPIYEKIALYKSGIIPV 116
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      67 TKMKCPGCGNSTITATNLCXPNMALPNSGCGWCPPLXHEPMSQPAWENTAVYQAGIIVP 126
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      117 MYRRVRCRSGIRFTINGHSYFNLVLTNVGAGADVHSVMKSGRTKQWLMRNMGOMV 176
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      127 NYKRPVQXRGSGIRFALISGHDFELVYTYTNVGGSGVVAQMSIKSGNTGMMASRNMGANW 186
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      177 QSNSTLNGQSLSFVYVTSIDRSVSVSENVAPPTW 209
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      187 QSNAYLAGQSLSFIVQDDGRKRYTAMNXPXNW 219
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 14

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US-08-845-539-6
; Sequence 6, Application US/0884539
; Patent No. 5929303
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,539
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-078200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-845-539-6

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Query Match          52.4%; Score 630.5; DB 2; Length 179;
Best Local Similarity 65.5%; Pred. No. 6,3e-63;
Matches 116; Conservative 16; Mismatches 36; Indels 9; Gaps 2;

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Oy      10 ATFEYXXGDAAXXTMGACGYNLVSGYGLFETALSTALFDQGLSCGACXELMCVNDPWC 69
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      3 ATFEYXXGDAAXXTMGACGYNLVSGYGLFETALSTALFDQGLSCGACXELMCVNDPWC 62
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      70 IKGR-STIVTATNFCPP-----GGACDPNNHFDLSQPIYEKIALYKSGIIPWYRR 120
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      63 HPGSPCIFATNFCPPNFALPNDNGWCWLPRTDFDLAMPFLKIAEYRAGIGPVSYRR 122
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      121 VPKRSGIRFTINGHSYFNLVLTNVGAGADVHSVMKSGRTKQWLMRNMGOMV 177
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      123 VPKRSGIRFTINGHSYFNLVLTNVGAGADVHSVMKSGRTKQWLMRNMGOMV 179
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 15

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US-09-362-642-6
; Sequence 6, Application US/09362642
; Patent No. 6350935
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
; FILE REFERENCE: 023070-078210US
; CURRENT APPLICATION NUMBER: US/09/362,642
; CURRENT FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6

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US-08-440-517A-4
: Sequence 4, Application US/08440517A
: Patent No. 5959082
: GENERAL INFORMATION:
: APPLICANT: COSGROVE, DANIEL J.;
: APPLICANT: GUILTINAN, MARK;
: APPLICANT: SCHERRAN, TATYANA;
: APPLICANT: SHI, JUN
: TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
: ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
: STREET: 113 TECHNOLOGY CENTER
: CITY: UNIVERSITY PARK
: STATE: PENNSYLVANIA
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 16802-7000
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK
: COMPUTER: NEC 286
: OPERATING SYSTEM: DOS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/440,517A
: FILING DATE:
: CLASSIFICATION: 530
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 227
: TYPE: AMINO ACID
: TOPOLOGY: UNKNOWN
: US-08-440-517A-4

Query Match 53.9%; Score 649; DB 2; Length 227;
Best Local Similarity 57.7%; Pred. No. 7.3e-65;
Matches 122; Conservative 25; Mismatches 55; Indels 10; Gaps 3;

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QY 181 YLNGQSLSFVVTTSDRSRVSVFNVAPPPTWSFGQTYTGCGFRY 222
DB 181 YLNGQSLSFVVTTSDRSRVSVFNVAPPPTWSFGQTYTGCGFRY 222

RESULT 2

US-09-092-160-3
Sequence 3, Application US/09092160C
Patent No. 6255466
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Gullitman, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C11AUS3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 222
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: UNSURE
LOCATION: (14)..(58)
OTHER INFORMATION: Xaa 1s unknown or other.
US-09-092-160-3

Query Match 99.2%; Score 1194; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 6, 1e-126;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HMGFWINAHATFYXXGDAXXYTMGACGYNLXSQGYGLETAALSTALFDGSLGACXEL 60
DB 1 HMGFWINAHATFYXXGDAXXYTMGACGYNLXSQGYGLETAALSTALFDGSLGACXEL 60
QY 61 MCVNDPQWCKIKRSIVYATNFECPPGACDPNNHFDLSQPIYEKIALYKSGIIPWYRR 120
DB 61 MCVNDPQWCKIKRSIVYATNFECPPGACDPNNHFDLSQPIYEKIALYKSGIIPWYRR 120
QY 121 VRCKRSGIRFTINGHSYFNLYVTNNGAGADVHSYMSKSRKQWOLMSRNNQONSNS 180
DB 121 VRCKRSGIRFTINGHSYFNLYVTNNGAGADVHSYMSKSRKQWOLMSRNNQONSNS 180
QY 181 YLNGQSLSFVVTTSDRSRVSVFNVAPPPTWSFGQTYTGCGFRY 222
DB 181 YLNGQSLSFVVTTSDRSRVSVFNVAPPPTWSFGQTYTGCGFRY 222

RESULT 3

US-08-440-517A-2
Sequence 2, Application US/08440517A
Patent No. 5939082
GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.
APPLICANT: GULLITMAN, MARK;
APPLICANT: SCHERBAN, TATYANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
ADDRESS: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 228
TYPE: AMINO ACID
TOPOLOGY: UNKNOWN
US-08-440-517A-2

Query Match 74.6%; Score 898.5; DB 2; Length 228;
Best Local Similarity 72.2%; Pred. No. 8, 2e-93;
Matches 164; Conservative 19; Mismatches 35; Indels 9; Gaps 2;

QY 3 GPMINAHATFYXXGDAXXYTMGACGYNLXSQGYGLETAALSTALFDGSLGACXELMC 62
DB 3 GPMINAHATFYXXGDAXXYTMGACGYNLXSQGYGLETAALSTALFDGSLGACXELMC 62
QY 63 VNDPQWCKIKRSIVYATNFECPP-----GGACDPNNHFDLSQPIYEKIALYKSGI 114
DB 63 QNDGKWCILPG-SLYVTATNFECPPNNALPNNAGCWCNPPQGHFDLSQPIYQRIAGYRACIV 121
QY 115 PYWRYRRCRSGIRFTINGHSYFNLYVTNNGAGADVHSYMSKSRKQWOLMSRNNQO 174
DB 122 PYWRYRRCRSGIRFTINGHSYFNLYVTNNGAGADVHSYMSKSRKQWOLMSRNNQO 181
QY 175 NMQNSYLNQGSLSFVVTTSDRSRVSVFNVAPPPTWSFGQTYTGCGFR 221
DB 182 NMQNSYLNQGSLSFVVTTSDRSRVSVFNVAPPPTWSFGQTYTGCGFR 228

RESULT 4
US-09-092-160-2
Sequence 2, Application US/09092160C
Patent No. 6255466

GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Gullitman, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C11AUS3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 228
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: rice expansin

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DD 39 G6W1NAHA1F1UGSDASGIMGACUIGNLISQUGIGINIAALSTALFNNGLSGSCI EIRC 98

; CURRENT APPLICATION NUMBER: 05/09/011,232C

LENGTH: 249
TYPE: PRT
ORGANISM: Arabidopsis thaliana

QY 3 GPMINHAHAEFYXXGDDXXHMGAGCYGGLYSQGIETLALSTALPDQGLSCGACXEIIMC 62

Dd 24 GGMINHAHAEFYGGDASGSTMGACGICGLNLSQGIETLALSTALPDQGLSCGACFEIIRC 83

QY 63 VNDPQWICIGRSTIVYATNFCPP-----GGACDPNHHPLSPDITAEKALYKSGIT 11

Dd 84 ENDGKKMCLGP - SILVYATNFCPPNNALANNNGCMCPLEHEDLPQWFEQRIADQRAIV 14

QY 115 PVYVRRVRCRKRSGGIRFTINHSYFNLVLVTNNGAGADVHSYMKSGRTKQMLSRNNGO 17

Dd 143 PVSTRVRCRRRGGIRFTINHSYFNLVLITNNGAGADVHSAIINGSRIVQMSRNNGO 20

QY 175 NMQNSNYLNGGLSPVYVTSDRSVSYFENAPRTMSFGOTTYGGQFR 221

Dd 203 NMQNSNYLNGGLSPVYVTSDRSVSYFENAPRTMSFGOTTYGGQFR 249

RESULT 11
US-09-595-329A-2001
; Sequence 2001, Application US/09595329A

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Query Match          99.2%; Score 1194; DB 22; Length 222;
Best Local Similarity 100.0%; Pred. No. 1,8e-119;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HMGPMINAHATFYXXGDAXXTMGACGYGNLYSOGYGLTALSTALFDQGLSCGACXEL 60
    |||||||
DB 1 HMGPMINAHATFYXXGDAXXTMGACGYGNLYSOGYGLTALSTALFDQGLSCGACXEL 60
OY 61 MCNDPOMCIGKRSIVTATNFCPPGACDPNNHFDLSQPIYEKIALYKSGIIPMYRR 120
    |||||||
DB 61 MCNDPOMCIGKRSIVTATNFCPPGACDPNNHFDLSQPIYEKIALYKSGIIPMYRR 120
OY 121 VRCKRSGGIRFTINGHSYFNLYLVTVNGAGADVHSYMKSGRTKQOLMSRMGQWMOQNS 180
    |||||||
DB 121 VRCKRSGGIRFTINGHSYFNLYLVTVNGAGADVHSYMKSGRTKQOLMSRMGQWMOQNS 180
OY 181 YLNGOSLSFVYTTSDRRSVSFVNAPPTWSFGQTYTGQGFY 222
    |||||||
DB 181 YLNGOSLSFVYTTSDRRSVSFVNAPPTWSFGQTYTGQGFY 222

RESULT 5
US-09-620-394B-4043
: Sequence 4043, Application US/09620394B
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai
: APPLICANT: BROVER, Vyacheslav
: TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
: FILE REFERENCE: 2750-1067P
: CURRENT APPLICATION NUMBER: US/09/620,394B
: CURRENT FILING DATE: 2000-07-21
: NUMBER OF SEQ ID NOS: 9131
: SEQ ID NO 4043
: LENGTH: 221
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1..221
: OTHER INFORMATION: xaa is any amino acid
: NAME/KEY: misc.feature
: LOCATION: 1..221
: OTHER INFORMATION: Ceres Seq. ID 1388406
US-09-620-394B-4043

Query Match          98.6%; Score 1187; DB 20; Length 221;
Best Local Similarity 97.7%; Pred. No. 9,9e-119;
Matches 216; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 MGFWINAHATFYXXGDAXXTMGACGYGNLYSOGYGLTALSTALFDQGLSCGACXEL 61
    |||||||
DB 1 MGFWINAHATFYXXGDAXXTMGACGYGNLYSOGYGLTALSTALFDQGLSCGACXEL 60
OY 62 CVNDPOMCIGKRSIVTATNFCPPGACDPNNHFDLSQPIYEKIALYKSGIIPMYRR 121
    |||||||
DB 61 CVNDPOMCIGKRSIVTATNFCPPGACDPNNHFDLSQPIYEKIALYKSGIIPMYRR 120
OY 122 RCKRSGGIRFTINGHSYFNLYLVTVNGAGADVHSYMKSGRTKQOLMSRMGQWMOQNS 181
    |||||||
DB 121 RCKRSGGIRFTINGHSYFNLYLVTVNGAGADVHSYMKSGRTKQOLMSRMGQWMOQNS 180
OY 182 YLNGOSLSFVYTTSDRRSVSFVNAPPTWSFGQTYTGQGFY 222
    |||||||
DB 181 YLNGOSLSFVYTTSDRRSVSFVNAPPTWSFGQTYTGQGFY 221

RESULT 6
US-09-620-394B-4044
: Sequence 4044, Application US/09620394B
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai
: APPLICANT: BROVER, Vyacheslav

```

```

: TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
: FILE REFERENCE: 2750-1067P
: CURRENT APPLICATION NUMBER: US/09/620,394B
: CURRENT FILING DATE: 2000-07-21
: NUMBER OF SEQ ID NOS: 9131
: SEQ ID NO 4044
: LENGTH: 201
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1..201
: OTHER INFORMATION: xaa is any amino acid
: NAME/KEY: misc.feature
: LOCATION: 1..201
: OTHER INFORMATION: Ceres Seq. ID 1388407
US-09-620-394B-4044

Query Match          91.0%; Score 1096; DB 20; Length 201;
Best Local Similarity 99.5%; Pred. No. 5,4e-109;
Matches 200; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 22 MGCAGYGNLYSOGYGLTALSTALFDQGLSCGACXELMCVNDPOMCIGKRSIVTATN 81
    |||||||
DB 1 MGCAGYGNLYSOGYGLTALSTALFDQGLSCGACXELMCVNDPOMCIGKRSIVTATN 60
OY 82 FCPREGACDPNNHFDLSQPIYEKIALYKSGIIPMYRRVRCKRSGIRFTINGHSYFN 141
    |||||||
DB 61 FCPREGACDPNNHFDLSQPIYEKIALYKSGIIPMYRRVRCKRSGIRFTINGHSYFN 120
OY 142 VLVTVNGAGADVHSYMKSGRTKQOLMSRMGQWMOQNSYLNGOSLSFVYTTSDRRSVS 201
    |||||||
DB 121 VLVTVNGAGADVHSYMKSGRTKQOLMSRMGQWMOQNSYLNGOSLSFVYTTSDRRSVS 180
OY 202 FVNAPPTWSFGQTYTGQGFY 222
    |||||||
DB 181 FVNAPPTWSFGQTYTGQGFY 201

RESULT 7
US-60-324-109-21420
: Sequence 21420, Application US/60324109
: GENERAL INFORMATION:
: APPLICANT: Cao, Yongwei
: APPLICANT: Edgerton, Michael D
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Liu, Jindong
: APPLICANT: Stein, Joshua
: TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
: FILE REFERENCE: 38-10(52726)B
: CURRENT APPLICATION NUMBER: US/60/324,109
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 33196
: SEQ ID NO 21420
: LENGTH: 247
: TYPE: PRT
: ORGANISM: Glycine max
: FEATURE:
: NAME/KEY: glycine max
US-60-324-109-21420

Query Match          83.4%; Score 1004.5; DB 26; Length 247;
Best Local Similarity 80.0%; Pred. No. 4,8e-99;
Matches 176; Conservative 22; Mismatches 21; Indels 1; Gaps 1;

OY 3 GPMINAHATFYXXGDAXXTMGACGYGNLYSOGYGLTALSTALFDQGLSCGACXEL 62
    |||||||
DB 29 GPMINAHATFYXXGDAXXTMGACGYGNLYSOGYGLTALSTALFDQGLSCGACXEL 88
OY 63 VNDPOMCIGKRSIVTATNFCPPGACDPNNHFDLSQPIYEKIALYKSGIIPMYRR 122
    |||||||
DB 89 VNDPOMCIGKRSIVTATNFCPPGACDPNNHFDLSQPIYEKIALYKSGIIPMYRR 147

```

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Db 12 HMGPMINAHATFYGGDASGTMGACGYGNYSGYGLFETALSTALFDQGLSCGACFEL 71
QY 61 MCVNDPQMCIKGRSIVVTATNFCPPGACDPPNHFFDLSPYIEKIALYKSGIIPVWYR 120
Db 72 MCVNDPQMCIKGRSIVVTATNFCPPGACDPPNHFFDLSPYIEKIALYKSGIIPVWYR 131
QY 121 VRCKRSGGIRFTINGHSYFNLVLTNVGAGDVHSVSMKGSRTKQMLSRMGNQMNQNS 180
Db 132 VRCKRSGGIRFTINGHSYFNLVLTNVGAGDVHSVSMKGSRTKQMLSRMGNQMNQNS 191
QY 181 YLNGOSLSFVVTSDRRSVSFNVAPPTWSFGQTYTGQFRY 222
Db 192 YLNGOSLSFVVTSDRRSVSFNVAPPTWSFGQTYTGQFRY 233

```

RESULT 2

```

US-09-112-498A-9
Sequence 9, Application US/09112498A

```

GENERAL INFORMATION:

```

APPLICANT:
TITLE OF INVENTION: MICROBIAL SMOLLENIN PROTEIN, DNA SEQUENCES
TITLE OF INVENTION: ENCODING SUCH SMOLLENINS AND METHOD OF PRODUCING SUCH
NUMBER OF INVENTION: SMOLLENINS
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/112,498A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 98/14226
FILING DATE:
APPLICATION NUMBER: US 08/893,766
FILING DATE: 11-JUL-1997
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-112-498A-9

```

```

Query Match 99.3%: Score 1195; DB 15; Length 233;
Best Local Similarity 97.7%: Pred. No. 1.5e-119;
Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 HMGPMINAHATFYXXGDAAXXTMGACGYGNYSGYGLFETALSTALFDQGLSCGACFEL 60
Db 12 HMGPMINAHATFYGGDASGTMGACGYGNYSGYGLFETALSTALFDQGLSCGACFEL 71
QY 61 MCVNDPQMCIKGRSIVVTATNFCPPGACDPPNHFFDLSPYIEKIALYKSGIIPVWYR 120
Db 72 MCVNDPQMCIKGRSIVVTATNFCPPGACDPPNHFFDLSPYIEKIALYKSGIIPVWYR 131
QY 121 VRCKRSGGIRFTINGHSYFNLVLTNVGAGDVHSVSMKGSRTKQMLSRMGNQMNQNS 180
Db 132 VRCKRSGGIRFTINGHSYFNLVLTNVGAGDVHSVSMKGSRTKQMLSRMGNQMNQNS 191
QY 181 YLNGOSLSFVVTSDRRSVSFNVAPPTWSFGQTYTGQFRY 222
Db 192 YLNGOSLSFVVTSDRRSVSFNVAPPTWSFGQTYTGQFRY 233

```

RESULT 3

```

US-09-620-394B-4042
Sequence 4042, Application US/09620394B

```

GENERAL INFORMATION:

```

APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

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TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 4042
LENGTH: 255
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..255
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc-feature
LOCATION: 1..255
OTHER INFORMATION: Ceres Seq. ID 1388405
US-09-620-394B-4042

```

```

Query Match 99.3%: Score 1195; DB 20; Length 255;
Best Local Similarity 97.7%: Pred. No. 1.6e-119;
Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 HMGPMINAHATFYXXGDAAXXTMGACGYGNYSGYGLFETALSTALFDQGLSCGACFEL 60
Db 34 HMGPMINAHATFYGGDASGTMGACGYGNYSGYGLFETALSTALFDQGLSCGACFEL 93
QY 61 MCVNDPQMCIKGRSIVVTATNFCPPGACDPPNHFFDLSPYIEKIALYKSGIIPVWYR 120
Db 94 MCVNDPQMCIKGRSIVVTATNFCPPGACDPPNHFFDLSPYIEKIALYKSGIIPVWYR 131
QY 121 VRCKRSGGIRFTINGHSYFNLVLTNVGAGDVHSVSMKGSRTKQMLSRMGNQMNQNS 180
Db 154 VRCKRSGGIRFTINGHSYFNLVLTNVGAGDVHSVSMKGSRTKQMLSRMGNQMNQNS 213
QY 181 YLNGOSLSFVVTSDRRSVSFNVAPPTWSFGQTYTGQFRY 222
Db 214 YLNGOSLSFVVTSDRRSVSFNVAPPTWSFGQTYTGQFRY 255

```

RESULT 4

```

US-09-896-301-3
Sequence 3, Application US/09896301

```

GENERAL INFORMATION:

```

APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Gullclinn, Mark J
APPLICANT: Shcherban, Tatyana
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/896,301
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/092,160
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 08/440,517
PRIOR FILING DATE: 1995-05-12
PRIOR APPLICATION NUMBER: 08/242,090
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 222
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: rice expansin
NAME/KEY: UNSURE
LOCATION: (14)..(58)
OTHER INFORMATION: Xaa is unknown or other.
US-09-896-301-3

```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:56:50 : Search time 98.6303 Seconds
(without alignments)
792.249 Million cell updates/sec

Title: US-09-896-301-3

Perfect score: 1204
Sequence: 1 HMGPMINAHATFYXGXGAXX.....NVAPPTWFGGTYTGGRY 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents, AA, Main:*

- 1: /cgn2_6/ptodata/2/paa/US06.COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US07.COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US08.COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US081.COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US082.COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US083.COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US084.COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US085.COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US086.COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US087.COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US088.COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US089.COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US090.COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US091.COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/US092.COMB.pep.*
- 16: /cgn2_6/ptodata/2/paa/US093.COMB.pep.*
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- 20: /cgn2_6/ptodata/2/paa/US097.COMB.pep.*
- 21: /cgn2_6/ptodata/2/paa/US098.COMB.pep.*
- 22: /cgn2_6/ptodata/2/paa/US099.COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/US100.COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/US101.COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US102.COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US103.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1195	99.3	233	US-09-112-498-10	Sequence 10, Appl
2	1195	99.3	233	US-09-112-498-9	Sequence 9, Appl
3	1195	99.3	255	US-09-620-394B-4042	Sequence 4042, Ap
4	1194	99.2	222	US-09-896-301-3	Sequence 3, Appl
5	1187	98.6	221	US-09-620-394B-4043	Sequence 4043, Ap
6	1096	91.0	201	US-09-620-394B-4044	Sequence 4044, Ap
7	1004.5	83.4	247	US-60-324-109-21420	Sequence 21420, A

8	927.5	77.0	242	US-09-595-329A-2003	Sequence 2003, Ap
9	927.5	77.0	249	US-09-570-581A-1823	Sequence 1823, Ap
10	927.5	77.0	250	US-09-595-329A-2002	Sequence 2002, Ap
11	927.5	77.0	260	US-09-595-329A-2001	Sequence 2001, Ap
12	913.5	75.9	264	US-60-324-109-21386	Sequence 21386, A
13	909.5	75.5	237	US-09-112-498A-7	Sequence 7, Appl
14	909.5	75.5	254	US-09-071-252-37	Sequence 37, Appl
15	907.5	75.4	235	US-09-708-427-35961	Sequence 35961, A
16	907.5	75.4	248	US-09-708-427-35960	Sequence 35960, A
17	905.5	75.2	248	US-60-312-544-6608	Sequence 6608, Ap
18	904.5	75.1	236	US-09-595-329A-955	Sequence 955, Ap
19	904.5	75.1	250	US-09-595-328C-1913	Sequence 954, Ap
20	898.5	74.6	228	US-09-896-301-2	Sequence 2, Appl
21	898	74.6	236	US-09-112-498-4	Sequence 8, Appl
22	891.5	74.0	223	US-09-112-498A-3	Sequence 3, Appl
23	891.5	74.0	223	US-09-595-328C-1914	Sequence 1914, Ap
24	876.5	72.8	242	US-09-595-328C-1913	Sequence 1913, Ap
25	876.5	72.8	250	US-09-595-328C-1912	Sequence 1912, Ap
26	876.5	72.8	256	US-09-112-498-5	Sequence 5, Appl
27	870	72.3	222	US-60-324-109-22664	Sequence 22664, A
28	868.5	72.1	227	US-09-112-498A-5	Sequence 5, Appl
29	857.5	71.2	227	US-09-896-301-7	Sequence 7, Appl
30	857.5	71.2	227	US-09-708-427-1757	Sequence 1757, Ap
31	855.5	71.1	262	US-09-708-427-1756	Sequence 1756, Ap
32	855.5	71.1	273	US-09-410-191-6	Sequence 6, Appl
33	853.5	70.9	250	US-09-071-252-23	Sequence 6, Appl
34	853.5	70.9	250	US-09-071-252-23	Sequence 22, Appl
35	848.5	70.5	250	US-09-689-860-152	Sequence 152, Ap
36	842	69.9	253	US-09-708-427-35962	Sequence 35962, A
37	841.5	69.9	207	US-60-324-109-22976	Sequence 22976, A
38	838.5	69.6	273	US-09-112-498-14	Sequence 14, Appl
39	832.5	69.1	237	US-09-708-427-2083	Sequence 2083, Ap
40	832.5	69.1	257	US-09-112-498A-13	Sequence 13, Appl
41	832.5	69.1	258	US-09-595-329A-956	Sequence 956, Ap
42	828.5	68.8	207	US-09-112-498-6	Sequence 6, Appl
43	827.5	68.7	225	US-09-112-498-6	Sequence 8, Appl
44	823	68.4	232	US-09-112-498A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-112-498-10
Sequence 10, Application US/09112498
GENERAL INFORMATION:
APPLICANT: Swanson, Barbara A.
APPLICANT: Ward, Michael
APPLICANT: Penttila, Merja
APPLICANT: Jaakko, Pere
TITLE OF INVENTION: Microbially Swollen Protein, DNA Sequences Encoding Such Swollen Proteins and Method of Producing Such Swollen Proteins
FILE REFERENCE: GC378-2
CURRENT APPLICATION NUMBER: US/09/112,498
CURRENT FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 08/893,766
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 233
TYPE: PRT
ORGANISM: Plant/eukaryotic
US-09-112-498-10

Query Match 99.3%; Score 1195; DB 15; Length 233;
Best Local Similarity 97.7%; Pred. No. 1.5e-119;
Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
1 HMGPMINAHATFYXGXGAXXGTGACGCGYGLYSGYGLTAALSTLFDGSGCAGCXEL 60
|||||

Sun Oct 13 14:18:52 2002

us-09-896-301-3.rapn

Page 6

Oy	115	PWRYRVACRKSGGIRPTINHSFENILVLYNVCAGDVHSVSKSGRTKOLMSRMGO	174
Db	144	PVAYRVPVCVRGGIRPTINHSFENILVLYLITNVGAGDVHSAMVKGSRTOGMASRMWG	203
Oy	175	NMOSNLYNGOSLSFVYTTSPRBSVSNVAAPPMWSGQRYTGTGQFR	221
Db	204	NMOSNLYNGOSLSFVYTTSPGQITVSNVANNMAGMSGQITGTGQLR	250

Search completed: October 11, 2002, 15:15:44
Job time : 31.293 secs

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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..250
; OTHER INFORMATION: Ceres Seq. ID no. 3446951
US-09-935-625-23149
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Query Match
Best Local Similarity 75.5%; Score 909.5; DB 5; Length 250;
Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;
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QY 3 GPWNAHATFYXXGDAAXXTMGACGYNLSQGYGLTALSTALFDDGLSCGACXELMC 62
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 25 GGVNNAHATFYGGDASGTMGACGYNLSQGYGTNTALSTALFNNGLSGACFEIRC 84
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
QY 63 VNDPQWCIKRSIVTATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 85 QNDGKWCILPG-STIVTATNFCPPNNALPNNAGGWCNPPQOHFDLSQPVFGRIAYRAGIV 143
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
QY 115 PWAYRRVRCRSGGIRFTINGHSYFNLVLTNNGAGDVHSVMKSGRTKQWLMRNMQ 174
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 144 PWAYRRVRCRSGGIRFTINGHSYFNLVLTNNGAGDVHSAMVKSRTGQWAMSRMQ 203
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
QY 175 NMOSNLYNGQSLSFVYTTSDRSVVSFVNAPPTWSFGQTYTGQGR 221
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 204 NMOSNLYNGQSLSFVYTTSDGQTIYSNNVANAAGWSFGQTFGAQLR 250
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
```

```
RESULT 13
US-09-935-625-23153
; Sequence 23153, Application US/09935625
```

```
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 23153
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..250
; OTHER INFORMATION: Ceres Seq. ID no. 3446955
US-09-935-625-23153
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```
Query Match
Best Local Similarity 75.5%; Score 909.5; DB 5; Length 250;
Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;
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```
QY 3 GPWNAHATFYXXGDAAXXTMGACGYNLSQGYGLTALSTALFDDGLSCGACXELMC 62
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 25 GGVNNAHATFYGGDASGTMGACGYNLSQGYGTNTALSTALFNNGLSGACFEIRC 84
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
QY 63 VNDPQWCIKRSIVTATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 85 QNDGKWCILPG-STIVTATNFCPPNNALPNNAGGWCNPPQOHFDLSQPVFGRIAYRAGIV 143
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
QY 115 PWAYRRVRCRSGGIRFTINGHSYFNLVLTNNGAGDVHSVMKSGRTKQWLMRNMQ 174
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 144 PWAYRRVRCRSGGIRFTINGHSYFNLVLTNNGAGDVHSAMVKSRTGQWAMSRMQ 203
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
QY 175 NMOSNLYNGQSLSFVYTTSDRSVVSFVNAPPTWSFGQTYTGQGR 221
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 204 NMOSNLYNGQSLSFVYTTSDGQTIYSNNVANAAGWSFGQTFGAQLR 250
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
```

```
RESULT 14
US-09-935-625-31515
```

```
; Sequence 31515, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 31515
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..250
; OTHER INFORMATION: Ceres Seq. ID no. 3446951
US-09-935-625-31515
```

```
Query Match
Best Local Similarity 75.5%; Score 909.5; DB 5; Length 250;
Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;
```

```
QY 3 GPWNAHATFYXXGDAAXXTMGACGYNLSQGYGLTALSTALFDDGLSCGACXELMC 62
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 25 GGVNNAHATFYGGDASGTMGACGYNLSQGYGTNTALSTALFNNGLSGACFEIRC 84
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
QY 63 VNDPQWCIKRSIVTATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 85 QNDGKWCILPG-STIVTATNFCPPNNALPNNAGGWCNPPQOHFDLSQPVFGRIAYRAGIV 143
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
QY 115 PWAYRRVRCRSGGIRFTINGHSYFNLVLTNNGAGDVHSVMKSGRTKQWLMRNMQ 174
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 144 PWAYRRVRCRSGGIRFTINGHSYFNLVLTNNGAGDVHSAMVKSRTGQWAMSRMQ 203
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
QY 175 NMOSNLYNGQSLSFVYTTSDRSVVSFVNAPPTWSFGQTYTGQGR 221
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 204 NMOSNLYNGQSLSFVYTTSDGQTIYSNNVANAAGWSFGQTFGAQLR 250
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
```

```
RESULT 15
US-09-935-625-31519
; Sequence 31519, Application US/09935625
```

```
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 31519
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..250
; OTHER INFORMATION: Ceres Seq. ID no. 3446955
US-09-935-625-31519
```

```
Query Match
Best Local Similarity 75.5%; Score 909.5; DB 5; Length 250;
Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;
```

```
QY 3 GPWNAHATFYXXGDAAXXTMGACGYNLSQGYGLTALSTALFDDGLSCGACXELMC 62
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 25 GGVNNAHATFYGGDASGTMGACGYNLSQGYGTNTALSTALFNNGLSGACFEIRC 84
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
QY 63 VNDPQWCIKRSIVTATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 85 QNDGKWCILPG-STIVTATNFCPPNNALPNNAGGWCNPPQOHFDLSQPVFGRIAYRAGIV 143
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
```

Db 130 PVATRRVPCVRRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRFGQTFGAQLR 189
Qy 175 NMOSNSTYLNQGSLSFVYVTTSDRSVSVFNAPPTWSFGQTYTGQFR 221
Db 190 NMOSNSTYLNQGSLSFKYVTTSDGQTIYSNNVANAGMSFGQTFGAQLR 236

RESULT 9

US-09-935-625-31520
Sequence 31520, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 31520
LENGTH: 236
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..236
OTHER INFORMATION: Ceres Seq. ID no. 3446956
US-09-935-625-31520

Query Match 75.5%; Score 909.5; DB 5; Length 236;
Best Local Similarity 73.1%; Pred. No. 7, 1e-88;
Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;

Qy 3 GPVINAHAATFYXXGDAAXXTMGACGYGNLYSGYGLFETALSTALFPOGLSCGACXELMC 62
Db 11 GGVNAHAATFYGGDASGTMGACGYGNLYSGYGTNTALSTALFNNGLSCGACFEIRC 70
Qy 63 VNDPQWCIKGRSIVYATNFCPP-----GGACDPNHHFDLSQPIYKIALYKSGIT 114
Db 71 QNDGKWCPLPG-SIVYATNFCPPNNALPNNAGWCNPPQGHFDLSQPIYKIALYKSGIT 129
Qy 115 PVMYRRVRCRKGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRFGQTYTGQFR 174
Db 130 PVATRRVPCVRRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRFGQTYTGQFR 189
Qy 175 NMOSNSTYLNQGSLSFVYVTTSDRSVSVFNAPPTWSFGQTYTGQFR 221
Db 190 NMOSNSTYLNQGSLSFKYVTTSDGQTIYSNNVANAGMSFGQTFGAQLR 236

RESULT 10

US-09-935-625-2249
Sequence 2249, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 2249
LENGTH: 250
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..250
OTHER INFORMATION: Ceres Seq. ID no. 3446951
US-09-935-625-2249

Query Match 75.5%; Score 909.5; DB 5; Length 250;
Best Local Similarity 73.1%; Pred. No. 7, 6e-88;
Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;

Qy 3 GPVINAHAATFYXXGDAAXXTMGACGYGNLYSGYGLFETALSTALFPOGLSCGACXELMC 62
Db 25 GGVNAHAATFYGGDASGTMGACGYGNLYSGYGTNTALSTALFNNGLSCGACFEIRC 84
Qy 63 VNDPQWCIKGRSIVYATNFCPP-----GGACDPNHHFDLSQPIYKIALYKSGIT 114
Db 85 QNDGKWCPLPG-SIVYATNFCPPNNALPNNAGWCNPPQGHFDLSQPIYKIALYKSGIT 143
Qy 115 PVMYRRVRCRKGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRFGQTYTGQFR 174
Db 144 PVATRRVPCVRRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRFGQTYTGQFR 203
Qy 175 NMOSNSTYLNQGSLSFVYVTTSDRSVSVFNAPPTWSFGQTYTGQFR 221
Db 204 NMOSNSTYLNQGSLSFKYVTTSDGQTIYSNNVANAGMSFGQTFGAQLR 250

RESULT 11

US-09-935-625-2253
Sequence 2253, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 2253
LENGTH: 250
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..250
OTHER INFORMATION: Ceres Seq. ID no. 3446955
US-09-935-625-2253

Query Match 75.5%; Score 909.5; DB 5; Length 250;
Best Local Similarity 73.1%; Pred. No. 7, 6e-88;
Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;

Qy 3 GPVINAHAATFYXXGDAAXXTMGACGYGNLYSGYGLFETALSTALFPOGLSCGACXELMC 62
Db 25 GGVNAHAATFYGGDASGTMGACGYGNLYSGYGTNTALSTALFNNGLSCGACFEIRC 84
Qy 63 VNDPQWCIKGRSIVYATNFCPP-----GGACDPNHHFDLSQPIYKIALYKSGIT 114
Db 85 QNDGKWCPLPG-SIVYATNFCPPNNALPNNAGWCNPPQGHFDLSQPIYKIALYKSGIT 143
Qy 115 PVMYRRVRCRKGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRFGQTYTGQFR 174
Db 144 PVATRRVPCVRRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRFGQTYTGQFR 203
Qy 175 NMOSNSTYLNQGSLSFVYVTTSDRSVSVFNAPPTWSFGQTYTGQFR 221
Db 204 NMOSNSTYLNQGSLSFKYVTTSDGQTIYSNNVANAGMSFGQTFGAQLR 250

RESULT 12

US-09-935-625-23149
Sequence 23149, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 23149
LENGTH: 250

FEATURE:
 NAME/KEY: peptide
 LOCATION: 1..236
 OTHER INFORMATION: Ceres Seq. ID no. 3446956
 US-09-935-625-2254

Query Match 75.5%; Score 909.5; DB 5; Length 236;
 Best Local Similarity 73.1%; Pred. No. 7.1e-88;
 Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;

QY 3 GPWVNAHATFYXXGDAAXXTMGACGYGNLYSGYGLTALSTALFDQGLSCGACXELMC 62
 DB 11 GGVVNAHATFYGGDASGTMGACGYGNLYSGYGTNTALSTALFNNGLSCGACFEIRC 70
 QY 63 VNDPQWCKRGSIYVATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
 DB 71 QNDGKWCPLPG-SIVVTATNFCPPNNALPNNAGGMCNPPQOHFDLSQPIYRIADYRAGIV 129
 QY 115 PVMYRRVRCRSGIRFTINGHSYFNLVLTNVGAGDVHSVSKSGRTKQWLMSSRMWQ 174
 DB 130 PVAIRRVPCVRGIRFTINGHSYFNLVLTNVGAGDVHSAMVKSRTGQWQAMSSRMWQ 189
 QY 175 NMOSNSYLNGOSLSFVYTTSDRSVSVFNVAAPTWSFGQTYTGQFR 221
 DB 190 NMOSNSYLNGOSLSFVYTTSDGQTIYSNNVANAGMSFGQTFGTGAQLR 236

RESULT 6
 US-09-935-625-23150
 ; Sequence 23150, Application US/09935625

GENERAL INFORMATION:
 APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
 FILE REFERENCE: 2750-1481P
 CURRENT APPLICATION NUMBER: US/09/935,625
 CURRENT FILING DATE: 2001-08-24
 NUMBER OF SEQ ID NOS: 33136
 SEQ ID NO 23150
 LENGTH: 236
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: peptide
 LOCATION: 1..236
 OTHER INFORMATION: Ceres Seq. ID no. 3446952
 US-09-935-625-23150

Query Match 75.5%; Score 909.5; DB 5; Length 236;
 Best Local Similarity 73.1%; Pred. No. 7.1e-88;
 Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;

QY 3 GPWVNAHATFYXXGDAAXXTMGACGYGNLYSGYGLTALSTALFDQGLSCGACXELMC 62
 DB 11 GGVVNAHATFYGGDASGTMGACGYGNLYSGYGTNTALSTALFNNGLSCGACFEIRC 70
 QY 63 VNDPQWCKRGSIYVATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
 DB 71 QNDGKWCPLPG-SIVVTATNFCPPNNALPNNAGGMCNPPQOHFDLSQPIYRIADYRAGIV 129
 QY 115 PVMYRRVRCRSGIRFTINGHSYFNLVLTNVGAGDVHSVSKSGRTKQWLMSSRMWQ 174
 DB 130 PVAIRRVPCVRGIRFTINGHSYFNLVLTNVGAGDVHSAMVKSRTGQWQAMSSRMWQ 189
 QY 175 NMOSNSYLNGOSLSFVYTTSDRSVSVFNVAAPTWSFGQTYTGQFR 221
 DB 190 NMOSNSYLNGOSLSFVYTTSDGQTIYSNNVANAGMSFGQTFGTGAQLR 236

RESULT 7
 US-09-935-625-23154
 ; Sequence 23154, Application US/09935625
 ; GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
 FILE REFERENCE: 2750-1481P
 CURRENT APPLICATION NUMBER: US/09/935,625
 CURRENT FILING DATE: 2001-08-24
 NUMBER OF SEQ ID NOS: 33136
 SEQ ID NO 23154
 LENGTH: 236
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: peptide
 LOCATION: 1..236
 OTHER INFORMATION: Ceres Seq. ID no. 3446956
 US-09-935-625-23154

Query Match 75.5%; Score 909.5; DB 5; Length 236;
 Best Local Similarity 73.1%; Pred. No. 7.1e-88;
 Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;

QY 3 GPWVNAHATFYXXGDAAXXTMGACGYGNLYSGYGLTALSTALFDQGLSCGACXELMC 62
 DB 11 GGVVNAHATFYGGDASGTMGACGYGNLYSGYGTNTALSTALFNNGLSCGACFEIRC 70
 QY 63 VNDPQWCKRGSIYVATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
 DB 71 QNDGKWCPLPG-SIVVTATNFCPPNNALPNNAGGMCNPPQOHFDLSQPIYRIADYRAGIV 129
 QY 115 PVMYRRVRCRSGIRFTINGHSYFNLVLTNVGAGDVHSVSKSGRTKQWLMSSRMWQ 174
 DB 130 PVAIRRVPCVRGIRFTINGHSYFNLVLTNVGAGDVHSAMVKSRTGQWQAMSSRMWQ 189
 QY 175 NMOSNSYLNGOSLSFVYTTSDRSVSVFNVAAPTWSFGQTYTGQFR 221
 DB 190 NMOSNSYLNGOSLSFVYTTSDGQTIYSNNVANAGMSFGQTFGTGAQLR 236

RESULT 8
 US-09-935-625-31516
 ; Sequence 31516, Application US/09935625

GENERAL INFORMATION:
 APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
 FILE REFERENCE: 2750-1481P
 CURRENT APPLICATION NUMBER: US/09/935,625
 CURRENT FILING DATE: 2001-08-24
 NUMBER OF SEQ ID NOS: 33136
 SEQ ID NO 31516
 LENGTH: 236
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: peptide
 LOCATION: 1..236
 OTHER INFORMATION: Ceres Seq. ID no. 3446952
 US-09-935-625-31516

Query Match 75.5%; Score 909.5; DB 5; Length 236;
 Best Local Similarity 73.1%; Pred. No. 7.1e-88;
 Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;

QY 3 GPWVNAHATFYXXGDAAXXTMGACGYGNLYSGYGLTALSTALFDQGLSCGACXELMC 62
 DB 11 GGVVNAHATFYGGDASGTMGACGYGNLYSGYGTNTALSTALFNNGLSCGACFEIRC 70
 QY 63 VNDPQWCKRGSIYVATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
 DB 71 QNDGKWCPLPG-SIVVTATNFCPPNNALPNNAGGMCNPPQOHFDLSQPIYRIADYRAGIV 129
 QY 115 PVMYRRVRCRSGIRFTINGHSYFNLVLTNVGAGDVHSVSKSGRTKQWLMSSRMWQ 174


```

: GENERAL INFORMATION:
: APPLICANT: Cao, Yongwei
: APPLICANT: Edgerton, Michael D
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Liu, Jingdong
: APPLICANT: Stein, Joshua
: TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
: FILE REFERENCE: 38-10(52726)C
: CURRENT APPLICATION NUMBER: US/10/219,999
: PRIOR FILING DATE: 2002-08-15
: PRIOR APPLICATION NUMBER: US 60/324,109
: PRIOR FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: US 60/312,544
: PRIOR FILING DATE: 2001-08-15
: NUMBER OF SEQ ID NOS: 63520
: SEQ ID NO 59261
: LENGTH: 205
: TYPE: PRT
: ORGANISM: Glycine max
: US-10-219-999-59261

```

```

Query Match          79.1%; Score 952.5; DB 6; Length 205;
Best Local Similarity 81.1%; Pred. No. 1.7e-92;
Matches 167; Conservative 22; Mismatches 16; Indels 1; Gaps 1;

```

```

QY 17 DAXXMGACGAGYGNLYSGYGLTALSTALFDOGLSCGACXELMCVNDPOMCIRSRIV 76
   |||||||
Db 1 DASGTMGACGAGYGNLYSGYGTNTALSTALFNNGLSCGSCYQICANDPQCLMG-TIV 59
   |||||||
QY 77 VPAATNCPGACDPNNHFDLSOPRYEKIALYKSGIIPVVRVRCRKSIGIRFTINGH 136
   |||||||
Db 60 VPAATNCPGACDPNNHFDLSOPRYEQIAQIRAGIVVVRVRCRKSIGIRFTINGH 119
   |||||||
QY 137 STFNLYLVTVNAGAGDVHSVSKSGRTKQWLMNRNMGQMSNSYLNQSLSFVTTSDR 196
   |||||||
Db 120 SYFNLYLVTVNAGAGDVHSVSKSGRTKQWLMNRNMGQMSNSYLNQSLSFVTTSDR 179
   |||||||
QY 197 RSVSPFNAPRPMSPGQRTYTGQCFR 222
   |||||||
Db 180 RSVLSTNAPRPMSPGQRTYTGQCFR 205
   |||||||

```

```

RESULT 3
: US-10-219-999-42752
: Sequence 42752, Application US/10219999
: GENERAL INFORMATION:
: APPLICANT: Cao, Yongwei
: APPLICANT: Edgerton, Michael D
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Liu, Jingdong
: APPLICANT: Stein, Joshua
: TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
: FILE REFERENCE: 38-10(52726)C
: CURRENT APPLICATION NUMBER: US/10/219,999
: PRIOR FILING DATE: 2002-08-15
: PRIOR APPLICATION NUMBER: US 60/324,109
: PRIOR FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: US 60/312,544
: PRIOR FILING DATE: 2001-08-15
: NUMBER OF SEQ ID NOS: 63520
: SEQ ID NO 42752
: LENGTH: 264
: TYPE: PRT
: ORGANISM: Glycine max
: US-10-219-999-42752

```

```

Query Match          75.9%; Score 913.5; DB 6; Length 264;
Best Local Similarity 73.6%; Pred. No. 3.1e-88;
Matches 167; Conservative 19; Mismatches 32; Indels 9; Gaps 2;

```

```

QY 3 GPWINAHATFYXXGDAXXTMGACGYGNLYSGYGLTALSTALFDOGLSCGACXELMC 62

```

```

Db 39 GGWTNAHATFYXXGDAXXTMGACGYGNLYSGYGTNTALSTALFNNGLSCGSCYEIRK 98
   |||||||
QY 63 VNDPOMCIRKSIVTATNFCPP-----GCADPPNNHFDLSOPRYEKIALYKSGII 114
   |||||||
Db 99 ANDHRMCLPG-SIVYTATNFCPPNNALPNNNGKCNPLQHDLDQAPFLRIAYKAGIV 157
   |||||||
QY 115 PVMYRRVRCRKSIGIRFTINGHSYFNLYLVTVNAGAGDVHSVSKSGRTKQWLMNRNMGQ 174
   |||||||
Db 158 PVMYRRVRCRKSIGIRFTINGHSYFNLYLVTVNAGAGDVHSVSKSGRTKQWLMNRNMGQ 217
   |||||||
QY 175 NMOSNSYLNQSLSFVTTSDRSYVSFNAPRPMSPGQRTYTGQCFR 221
   |||||||
Db 218 NMOSNSYLNQSLSFVTTSDRSYVSFNAPRPMSPGQRTYTGQCFR 264
   |||||||

```

```

RESULT 4
: US-09-935-625-2250
: Sequence 2250, Application US/09935625
: GENERAL INFORMATION:
: APPLICANT: N. ALEXANDROV et al.
: TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
: FILE REFERENCE: 2750-1481P
: CURRENT APPLICATION NUMBER: US/09/935,625
: CURRENT FILING DATE: 2001-08-24
: NUMBER OF SEQ ID NOS: 33136
: SEQ ID NO 2250
: LENGTH: 236
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: NAME/KEY: peptide
: LOCATION: 1..236
: OTHER INFORMATION: Ceres Seq. ID no. 3446952
: US-09-935-625-2250

```

```

Query Match          75.5%; Score 909.5; DB 5; Length 236;
Best Local Similarity 73.1%; Pred. No. 7.1e-88;
Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;

```

```

QY 3 GPWINAHATFYXXGDAXXTMGACGYGNLYSGYGLTALSTALFDOGLSCGACXELMC 62
   |||||||
Db 11 GGWINAHATFYXXGDAXXTMGACGYGNLYSGYGTNTALSTALFNNGLSCGACFEIRK 70
   |||||||
QY 63 VNDPOMCIRKSIVTATNFCPP-----GCADPPNNHFDLSOPRYEKIALYKSGII 114
   |||||||
Db 71 QNDGKWLPG-SIVYTATNFCPPNNALPNNAGCNCPPQHFDSQVFORIAQYRAGIV 129
   |||||||
QY 115 PVMYRRVRCRKSIGIRFTINGHSYFNLYLVTVNAGAGDVHSVSKSGRTKQWLMNRNMGQ 174
   |||||||
Db 130 PVMYRRVRCRKSIGIRFTINGHSYFNLYLVTVNAGAGDVHSVSKSGRTKQWLMNRNMGQ 189
   |||||||
QY 175 NMOSNSYLNQSLSFVTTSDRSYVSFNAPRPMSPGQRTYTGQCFR 221
   |||||||
Db 190 NMOSNSYLNQSLSFVTTSDRSYVSFNAPRPMSPGQRTYTGQCFR 236
   |||||||

```

```

RESULT 5
: US-09-935-625-2254
: Sequence 2254, Application US/09935625
: GENERAL INFORMATION:
: APPLICANT: N. ALEXANDROV et al.
: TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
: FILE REFERENCE: 2750-1481P
: CURRENT APPLICATION NUMBER: US/09/935,625
: CURRENT FILING DATE: 2001-08-24
: NUMBER OF SEQ ID NOS: 33136
: SEQ ID NO 2254
: LENGTH: 236
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana

```

RESULT 2
US-10-219-999-59261
; Sequence 59261, Application US/10219999

Sun Oct 13 14:18:53 2002

us-09-896-301-3.rpr

Page 6

Search completed: October 11, 2002, 15:00:59
Job time : 11.141 secs

C:Superfamily: expansin

Query Match 69.1%; Score 842; DB 2; Length 253;

Best Local Similarity 67.4%; Pred. No. 2.6e-71;

Matches 153; Conservative 27; Mismatches 37; Indels 10; Gaps 3;

QY 3 GPWINAHATFYXXGDAAXXTMGACGYNLVSOGYGLETALSTALFDQGLSCGACXELMC 62

DB 28 GGMGGHATFYGGEDASGTMGACGYNLVGGGYGTNTALSTALFNNGLTCGACYEMKC 87

QY 63 VNDPQWCKRSGIRSVYVATNFCPP-----GCACDPNNHFDLSQPIYKIALYKSGI 114

DB 88 NDDEPQWCL-GSTIVTATNFCPPNPDLNDNGWCNPPDLHFDLAEPAFLQIAQYRAGI 146

QY 115 PVMYRRVRCRSGIRFTINGHSYFNLYVTNNGAGDVHVSVMKSGSRK-WQLMSRNMG 173

DB 147 PVSRRRVRCRSGIRFTINGHSYFNLYVTNNGAGDVHVSVMKSGSRK-WQLMSRNMG 206

QY 174 QNMOSNSYLNGQSLSFVVTSDRRSVVSFNVAAPTWSFGQTYTGQFR 220

DB 207 QNMOSNSYLNGQSLSFVVTSDRRSVVSFNVAAPTWSFGQTYTGQFR 253

RESULT 13

DB4820

Probable expansin [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: D84820

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beaulieu, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

et al.; Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; M01D:20083487

A:Accession: D84820

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-257 <STO>

A:Cross-references: GB:AE002093; NID:g2795809; PIDN:AA97125.1; GSPDB:GND0139

A:Genetics:

A:Gene: At2g39700

A:Map position: 2

C:Superfamily: expansin

Query Match 69.1%; Score 832.5; DB 2; Length 257;

Best Local Similarity 65.8%; Pred. No. 2.1e-70;

Matches 150; Conservative 23; Mismatches 46; Indels 9; Gaps 2;

QY 3 GPWINAHATFYXXGDAAXXTMGACGYNLVSOGYGLETALSTALFDQGLSCGACXELMC 62

DB 29 GAWQNAHATFYGGSDASGTMGACGYNLVSOGYGTNTALSTALFNNGMSGACFEELMC 88

QY 63 VNDPQWCKRSGIRSVYVATNFCPP-----GCACDPNNHFDLSQPIYKIALYKSGI 113

DB 89 ANDPQWCKRSGIRSVYVATNFCPPNPDLNDNGWCNPPDLHFDLAEPAFLQIAQYRAGI 148

QY 114 IPMYRRVRCRSGIRFTINGHSYFNLYVTNNGAGDVHVSVMKSGSRK-WQLMSRNMG 173

DB 149 VPSTRRVRCRSGIRFTINGHSYFNLYVTNNGAGDVHVSVMKSGSRK-WQLMSRNMG 208

QY 174 QNMOSNSYLNGQSLSFVVTSDRRSVVSFNVAAPTWSFGQTYTGQFR 221

DB 209 QNMOSNAVLVGOALSFRVTSDBRSTSTSWNAPPSNMQFGQTYTGQFR 256

RESULT 14

SS3082

pollen allergen homolog, hypothetical (clone PPA1) - garden pea

C:Species: Pisum sativum (garden pea)

C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000

C:Accession: S65056; S53082

R:Michael, A.J.

Plant Mol. Biol. 30, 219-224, 1996

A:Title: A cDNA from pea petals with sequence similarity to pollen allergen, cytokin-

A:Reference number: S65056; M01D:96197414

A:Accession: S65056

A:Molecule type: mRNA

A:Residues: 1-258 <MI2>

A:Cross-references: EMBL:X85187; NID:g732904; PIDN:CA45470.1; PID:g732905

A:Note: submitted to the EMBL Data Library, March 1995

C:Superfamily: expansin

C:Keywords: pollen

Query Match 69.1%; Score 832.5; DB 2; Length 258;

Best Local Similarity 66.2%; Pred. No. 2.1e-70;

Matches 151; Conservative 25; Mismatches 43; Indels 9; Gaps 2;

QY 3 GPWINAHATFYXXGDAAXXTMGACGYNLVSOGYGLETALSTALFDQGLSCGACXELMC 62

DB 30 GPTWTAHATFYGGSDASGTMGACGYNLVSOGYGTNTALSTALFNNGLTCGACFEELMC 89

QY 63 VNDPQWCKRSGIRSVYVATNFCPP-----GCACDPNNHFDLSQPIYKIALYKSGI 113

DB 90 DDDPQWCKRSGIRSVYVATNFCPPNPDLNDNGWCNPPDLHFDLAEPAFLQIAQYRAGI 149

QY 114 IPMYRRVRCRSGIRFTINGHSYFNLYVTNNGAGDVHVSVMKSGSRK-WQLMSRNMG 173

DB 150 VVATRRVRCRSGIRFTINGHSYFNLYVTNNGAGDVHVSVMKSGSRK-WQLMSRNMG 209

QY 174 QNMOSNSYLNGQSLSFVVTSDRRSVVSFNVAAPTWSFGQTYTGQFR 221

DB 210 QNMOSNAVLVGOALSFRVTSDBRSTSTSWNAPPSNMQFGQTYTGQFR 257

RESULT 15

T47689

expansin-like protein - Arabidopsis thaliana

N:Alternate names: protein T22E16.160

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000

C:Accession: T47689

R:Benes, V.; Wurmbe, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer,

submitted to the Protein Sequence Database, February 2000

A:Reference number: Z24472

A:Accession: T47689

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-260 <BEN>

A:Cross-references: EMBL:AL132975

A:Experimental source: cultivar Columbia; BAC clone T22E16

C:Genetics:

A:Map position: 3

A:Introns: 52/1; 158/2

A:Note: T22E16.160

C:Superfamily: expansin

Query Match 68.6%; Score 825.5; DB 2; Length 260;

Best Local Similarity 64.5%; Pred. No. 9.5e-70;

Matches 147; Conservative 27; Mismatches 45; Indels 9; Gaps 2;

QY 3 GPWINAHATFYXXGDAAXXTMGACGYNLVSOGYGLETALSTALFDQGLSCGACXELMC 62

DB 32 GSWQTAHATFYGGSDASGTMGACGYNLVSOGYGTNTALSTALFNNGMSGACFEELMC 91

QY 63 VNDPQWCKRSGIRSVYVATNFCPP-----GCACDPNNHFDLSQPIYKIALYKSGI 113

DB 92 VNDPQWCKRSGIRSVYVATNFCPPNPDLNDNGWCNPPDLHFDLAEPAFLQIAQYRAGI 151

QY 114 IPMYRRVRCRSGIRFTINGHSYFNLYVTNNGAGDVHVSVMKSGSRK-WQLMSRNMG 173

DB 152 VPSTRRVRCRSGIRFTINGHSYFNLYVTNNGAGDVHVSVMKSGSRK-WQLMSRNMG 211

QY 174 QNMOSNSYLNGQSLSFVVTSDRRSVVSFNVAAPTWSFGQTYTGQFR 221

DB 212 QNMOSNAVLVGOALSFRVTSDBRSTSTSWNAPPSNMQFGQTYTGQFR 259

[illegible]

C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #extl_change 16-Feb-2001
C:Accession: F84831
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, B.;
Nuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487
A:Accession: F84831
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-223 <STO>
A:Cross-references: GB:AE002093; NID:92651297; PIDN:AB87577.1; GSPDB:GN00339
C:Genetics:
A:gene: AT2g40610
A:Map position: 2

1

A:Title: Molecular cloning and sequence analysis of expansins- α highly conserved, multi
A:Reference number: Z14894; MUID:96010146
A:Accession: J50654
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-237 <SHC>
A:Cross-references: EMBL:U30476; PIDN:AAB38070.1
C:Genetics:
A:Gene: EXP1
C:Function:
A:Description: Induces extension (creep) in plant cell walls
C:Superfamily: expansin
C:Keywords: cell wall

Query Match	75.5%	Score	909.5	DB 2	Length	237			
Best Local Similarity	73.1%	Pred	No. 1.2e-77						
Matches	166	Conservative	19	Mismatches	33	Indels	9	Gaps	2

[illegible]

C84444
probable expansin [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: C84444
R:Lin, X.; Kall, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii,
M.; Koo, H.; Molitor, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tai,
neus, D.; Nlemane, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; V
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
A:Reference number: AB4420; MUID:20083487
A:Accession: C84444
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-248 <SRO>
A:Cross-references: CR:AE002093; NID:g34c1833; PIDN:AMC32927.1; GSPDB:GN00139
C:Genetics
A:Gene: At2g03090
A:Map position: 2
C:Superfamily: expansin

Query Match	75.48	Score	907.5	DB	2	length	248
Best Local Similarity	72.48	Pred. No.	1.9e-77				
Matches	163	Conservative	24	Mismatches	29	Indels	9
						Gaps	2

[illegible]

Qy 177 QNSNYLNGQSLFVYVTTSDRSKVSINAVPPTMSFGQTYTCGQFR 221
 111: 1111:111 11 11:111 1:1 111111:11 111
 Db 204 QSNLLNGQSLFVYVTTASDGRVTSNNIAPASWSFGQTFYTGQFR 248

RESULT 4
T09821
expansin (clone pTexp3) - loblolly pine (fragment)

C/Species: *Salmonella enterica* serovar *Senftenberg*
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C/Accession: F709821
R/Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
Submitted to the EMBL Data Library, July 1996
#Sequence_Revision: 1
#Text_Change: 1

A:Description: Expansins are conserved in conifers and expressed in response to exogenous ABA
A:Reference number: Z16866

A:Accession: 1098821
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64891, NID:q1778100; PID:q1778101
A:Experimental source: clone pctxp3
C:Superfamily: expnsin

Query Match	72.3%	Score	870.5	DB	2	Length	232
Best Local Similarity	69.8%	Pred	No	5.1e-74			
Matches	157	Conservative	23	Mismatches	36	Indels	9
						Gaps	2

Qy 3 GPMINAHATFFYXXGDAAXXTMGACAGCGYNLYSGCYGLETAALSTALFPDGLSCGCACXELMC 62
| : ||||| | | ||||||||| | ||||| : ||||| : |
Db 8 GGMESHATFFYGSDASGTMGACAGCGYNLYSGCYGTNTAALSTALFNDGLSCGCACYEMRC 67

QY 63 VNDPWCICKGRSIVVTATNFCPP-----GGACDPDHHFDSQPIYEKIALYKSGI 114
:||||:|::| ||||| | ||| ||||::| |||::| |:
Db 68 NDDPQWCLPG-TVTYATNTECPNNALPDNGGWCNPLQHFMAEPAFLKIAYRGIV 126

```

Oy 115 PMVRRVCRKRGSGIREFTINGHSYENLVLTNNGAGDVHVSNAKGSPTKQWLSRNMGO 174
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 127 PLTYRVPCLKKGGIRFTVNGHSYENLVLTNNGAGDVHVAISIKGSRGQWQPMRSRNMGO 186

```

QY	175	NMQSNSY	LNQSL	FEVY	TTSD	RKRSV	SENV	APTWS	FGQTY	GCQ	213
				:			:		:		
Db	187	NMQSNSY	LNQSL	SFQY	TTSD	GRVSV	NNVAP	SNMQ	FGQTF	EGSQ	231

RESULT 5
T09826

C:Species: Pinus taeda (loblolly pine)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09826

A:Description: Expansins are conserved in conifers and expressed in response to exoge
A:Reference number: Z16866

A;Accession: U00000
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-232 <HUT>

A:Cross-references: EMBL:U64893; NID:g17778104; PID:g1778105
A:Experimental source: clone pTexp5
C:Superfamily: expansin

Query Match	71.88	Score	864.5	DB	2	Length	232
Best Local Similarity	69.38	Pred. No.	1.9e-73				
Matches	156	Conservative	24	Mismatches	36	Indels	9
						Gaps	2

QY 3 GPTINAHATFYXXGDAAXXTMGAGCYGNLSQGYGLTALSTALFDDGLSGACXELMC 62
| : | | | | | | | | | | | | | | | | | | | | : |
DB 8 CGNESAHATFYCGSDASCTMGAGCYGNLSQGYGNTALSTALFNDGLSGACYEMQC 67

```
Oy      63 VNDPQWCTKGRSIVTATNCP-----GCACDPNNHFDLSQIYEKIALYKSGII.114  
        :|||||: |:: ||||| | | | | | | | | | | | | | | | | |  
Db      68 NDDPQWCPLPG-TVTATATNCPNNALPNDSGMCNPLOHFDMAEPAFLKIAKYRGCIV.120
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:53:05 ; Search time 11.141 Seconds

(without alignments)
1914.721 Million cell updates/sec

Title: US-09-896-301-3

Perfect score: 1204

Sequence: 1 HMGPMINAHATFYXXGDAAXX.....NVAPPTWSEFGQYTTGGQPRY 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71:*

SUMMARIES

Result No. Score Query Match Length DB ID Description

1	1195	99.3	255	2	T50655	expansin EXP5 [imp
2	909.5	75.5	237	2	T50654	expansin EXP1 [imp
3	907.5	75.4	248	2	C84444	probable expansin
4	870.5	72.3	232	2	T09821	expansin (clone pp
5	864.5	71.8	232	2	T09826	expansin (clone pp
6	863.5	71.7	232	2	T09818	expansin (clone pp
7	857.5	71.2	232	2	T10079	expansin SI precu
8	856.5	71.1	232	2	T09825	expansin (clone pp
9	855.5	71.1	262	2	T02530	probable expansin
10	852.5	70.8	258	2	T09786	expansin - upland
11	845.5	70.2	258	2	T48247	expansin - like prot
12	842	69.9	253	2	T84831	probable expansin
13	832.5	69.1	257	2	D84820	expansin-1-like prot
14	832.5	69.1	258	2	S53082	probable expansin
15	825.5	68.6	260	2	T47689	pollen allergen ho
16	823	68.4	255	2	T50656	expansin-like prot
17	816.5	67.8	257	2	T50658	expansin EXP2 [imp
18	815.5	67.7	246	2	T04175	expansin 9 [import
19	805.5	66.9	251	2	T03258	expansin - rice
20	804.5	66.8	257	2	T02727	expansin 2 - rice
21	804.5	66.8	259	2	T50653	probable expansin
22	799.5	66.4	262	2	T50660	expansin EXP6 [imp
23	792.5	66.4	255	2	T06573	alpha-expansin 2 l
24	788.5	65.5	260	2	T08016	expansin 18 - toma
25	782.5	65.0	261	2	T07630	probable expansin
26	778.5	64.7	258	2	T10083	expansin 1 - tomat
27	776.5	64.5	264	2	T50659	expansin S2 precu
28	734.5	61.0	252	2	T86335	alpha-expansin OSE
29	727.5	60.4	255	2	T02010	hypothetical prote
						expansin homolog T

30	725	60.2	261	2	T03737	expansin - rice
31	698	58.0	255	2	T03299	expansin 3 - rice
32	624.5	51.9	257	2	G96654	hypothetical prote
33	620.5	51.5	257	2	F86259	protein T12C24.10
34	592.5	49.2	160	2	T09871	expansin - upland
35	548.5	45.6	256	2	T05648	expansin homolog F
36	278.5	23.1	259	2	T50657	expansin [imp
37	278.5	23.1	271	2	H84592	beta-expansin [imp
38	257.5	21.4	276	2	T09041	beta-expansin [imp
39	256	21.3	102	2	T09828	clm1 protein homol
40	252.5	21.0	277	2	S48032	expansin (clone pp
41	250	20.8	77	2	T09815	clm1 protein - soy
42	241	20.0	491	2	F96681	expansin (clone pp
43	237	19.7	261	2	T04301	protein F1E22.6 [i
44	225.5	18.7	263	2	S13614	beta-expansin - ri
45	224	18.6	259	2	E84886	major allergen Lol
						probable beta-expa

ALIGNMENTS

RESULT 1
T50655
expansin EXP5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C:Accession: T50655
R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gullitnan, M.J.; McQueen-Mason, S.J.; Shi
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
A:Reference number: 214894; MUID:96016146
A:Accession: T50655
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-255 <SHC>
A:Cross-references: EMBL:U30478; PTDN:AA38071.1
A:Experimental source: variety Columbia
A:Gene: Exps
C:Function:
A:Description: induces extension (creep) in plant cell walls
C:Superfamily: expansin
C:Keywords: cell wall

Query Match 99.3%; Score 1195; DB 2; Length 255;
Best Local Similarity 97.7%; Pred. No. 2; Se-104;
Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 HMGPMINAHATFYXXGDAAXXTMGACGCGYGNYSQYGLTAALSTALFDGLSCGACXEL 60
Db 34 HMGPMINAHATFYGGGADSGTMCACGCGYGNYSQYGLTAALSTALFDGLSCGACFEL 93

QY 61 MCVPDPWCICIGRSIVTATNFCPPGACDPNNHFDLSQPIYEKIALYKSGIIPVYRR 120
Db 94 MCVPDPWCICIGRSIVTATNFCPPGACDPNNHFDLSQPIYEKIALYKSGIIPVYRR 153

QY 121 VRCRSGGIPTINGHSYFNLYVTNNGAGDVHSYMKSRKTKWQMSRNQWQMSNS 160
Db 154 VRCRSGGIPTINGHSYFNLYVTNNGAGDVHSYMKSRKTKWQMSRNQWQMSNS 213

QY 181 YLNGQSLFFVYTTSDRRSVSFNVAPTWSEFGQYTTGGQPRY 222
Db 214 YLNGQSLFFVYTTSDRRSVSFNVAPTWSEFGQYTTGGQPRY 255

RESULT 2
T50654
expansin EXP1 [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C:Accession: T50654
R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gullitnan, M.J.; McQueen-Mason, S.J.; Shi
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995


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DR PROSITE; PS50004; C2_DOMAIN.2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM.1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM.2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM.1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat.
FT DOMAIN 22 71 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 86 135 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 157 244 C2 DOMAIN.
FT NP_BIND 320 578 PROTEIN KINASE.
FT BINDING 326 334 ATP (BY SIMILARITY).
FT BINDING 349 349 ATP (BY SIMILARITY).
FT ACT_SITE 444 444 BY SIMILARITY.
SQ SEQUENCE 649 AA; 74079 MW; A53253399284E330 CRC64;

Query Match 6.5%; Score 78; DB 1; Length 649;
Best Local Similarity 23.4%; Pred. No. 6.9;
Matches 41; Conservative 23; Mismatches 57; Indels 54; Gaps 11;

QY 30 NLVS---QVGLT-----AALSTALFDGGLSCGAC-----XELMCVNDP----- 66
Db 84 NLHFKLHSTSPFCHCGSLYGLHGLKCDSCDMNVHKRCKNVPLLCGTDHERR 143
QY 67 -----QWCIRGSIIV---TATNFCP---PGGACDPNNHFDLSQPIYKIALYKSGIIPV 116
Db 144 GRILIKGAVKSKVLELLEAKNLCPMDPNCLADP-----YVKVYL-----IPY 187
QY 117 MYRRVRCRSGIRFTINGHSYFNLVLTNNGAGDVHSVMKSGRTKQMLMSRN 171
Db 188 DAHLKLKLTITKASLN--PWNESFTVDIPEDNSKRUSLE--VWDWRTSRN 237

RESULT 15
TP2A_CHICK
ID TP2A.CHICK STANDARD; PRT; 1553 AA.
AC 042130;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA topoisomerase II, alpha isozyme (EC 5.99.1.3).
GN TP2A.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Nimi A., Harata M., Mizuno S.;
RT "Chicken DNA topoisomerase 2 alpha and beta."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; GENERALLY LOCATED IN THE
NUCLEOPLASM.
CC -1- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
RELAX ONLY NEGATIVE SUPERCOILS.
CC -1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
```

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CC -----
CC EMBL; AB007445; BAA22539.2; -.
DR HSSP; P06786; 1BGW.
DR InterPro; IPR003957; CBFA_NFYB_topis.
DR InterPro; IPR001241; DNA_topoisomI.
DR InterPro; IPR002205; DNA_topoisomIV.
DR InterPro; IPR003594; HATPase_C.
DR Pfam; PF00204; DNA_topoisomI.1.
DR Pfam; PF00521; DNA_topoisomIV.1.
DR Pfam; PF02518; HATPase_C.1.
DR PRINTS; PR00615; CCAATSUBUNTA.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD000616; DNA_topoisomI.1.
DR SMART; SM00387; HATPase_C.1.
DR SMART; SM00433; TOP2c.1.
DR SMART; SM00434; TOP4c.1.
DR PROSITE; PS00177; TOPOISOMERASE_II.1.
KW Isomerase; Topoisomerase; DNA-binding; ATP-binding; Nuclear protein.
FT NP_BIND 162 167 ATP (POTENTIAL).
FT ACT_SITE 806 DNA_CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 1553 AA; 174991 MW; 3322CE95238F71B2 CRC64;

Query Match 6.5%; Score 78; DB 1; Length 1553;
Best Local Similarity 21.9%; Pred. No. 18;
Matches 44; Conservative 30; Mismatches 81; Indels 46; Gaps 9;

QY 17 DAXXTMGACGYG---NLYSGVGLTAAALSTALFDGGLSCGACXELMCVNDPWCIC- 71
Db 155 DEKKVYGGRRGYCAKCNLFSTFTYET-----ACEYKKLKQWTDNM 199
QY 72 GRSIVTATNFCPPGGAC---DPPNHFDLSQPIYKIALYKSGIIPVRYR--CKRS 126
Db 200 GKAGEMTLKHFEDEYTCVTFQP---DLSK---FKMTILDKDIVALMSRRAYDIAGST 251
QY 127 GGIRFTING-----HSYFNLVLTNNGAGDVHSVMKSGRTKQMLMSRNQMS 178
Db 252 KDVKVFLNGKRLPLVYKFRSTVDLYLKDQVDFGNALKVHIEVNSRWEVCLTLSEKGFQO 311
QY 179 NSYLNGOSLSFVVTSDRRSV 199
Db 312 VSEFVNS-----IATTKGGRHV 327
```

Search completed: October 11, 2002, 14:57:30
 Job time : 6.73432 secs

DR PDB: 2PBH: 25-FEB-98.
 DR PDB: 3PBH: 25-FEB-98.
 DR MEROPS: C01.060: -.
 DR SWISS-2DPAGE: P07858; HUMAN.
 DR MIM: 116810: -.
 DR InterPro: IPR000668; Peptidase_C1.
 DR InterPro: IPR000169; Thiolprol_act_site.
 DR Pfam: PF00112; Peptidase_C1; 1.
 DR PRINTS: PR00705; PAPA1N.
 DR PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
 DR PROSITE: PS00640; THIOL_PROTEASE_ASN; 1.
 DR Hydrolase: Thiol protease; lysosome; glycoprotein; zymogen; signal;
 KW Polymorphism: 3D-structure.
 KM SIGNAL: 1 17
 FT PROPEP 18 79
 FT CHAIN 80 333
 FT CHAIN 80 126
 FT CHAIN 129 333
 FT PROPEP 334 339
 FT ACT_SITE 108 108
 FT ACT_SITE 278 278
 FT ACT_SITE 298 298
 FT ACT_SITE 93 122
 FT DISULFID 105 150
 FT DISULFID 141 207
 FT DISULFID 142 146
 FT DISULFID 179 211
 FT DISULFID 187 198
 FT CARBOHYD 192 192
 FT VARIANT 26 26
 FT CONFLICT 228 228
 FT SEQUENCE 339 AA: 37807 MW: 0605FE184AE47070 CAC64:
 N-LINKED (GLCNAC. . .).
 V -> L
 /FTID=VAR_006724.
 N -> D (IN REF 4).
 Query Match
 Best Local Similarity 19.8%; Pred. No. 0.9; Mismatches 44; Conservative 24; Indels 80; Gaps 10;

7.0%; Score 84; DB 1; Length 339;
 Query Match
 Best Local Similarity 19.8%; Pred. No. 0.9; Mismatches 44; Conservative 24; Indels 80; Gaps 10;
 Matches 44; Conservative 24; Indels 80; Gaps 10;
 DB 7 NAHATF-YXXGDAAXTWGACGYGNLYSGYGLT-----AALSTALFDGSLGACGX 58
 DB 126 NAHVSVEVSADLLTCCGSMCGDG--CNGCYPAEAMNFTKGLVSGGLYSHVGCRRPS 183
 QY 59 ELWC---VNDPOMCKIGRSIVTATNFCRPG-----GACDRPHHFDLSQPT 102
 DB 184 IPCEHHVNGSRPCTGEGTPEKSKICERGPYTKQDKHGYNSYSNSEKDIMAEI 243
 QY 103 YEK-----IALYKSGIIPVYRRVRCRKGSGIRFTINGHSYENLVLTNVGGA 150
 DB 244 YKNGPVEGAFSVSDPILYKSGV---YQHVTGEMMG----- 277
 QY 151 GDVHSVSMKG---SRTKQMLSRNMGONNSNSY---LNGQ 185
 DB 278 ---HAIRILGWGVENGTPYVLANSWMTDMGDNCFKILKQ 316

RESULT 12
 ID HRA1_MOUSE STANDARD: PRT: 480 AA.
 AC Q9RL18:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine protease HTRA1 precursor (EC 3.4.21.-).
 CN PRS11 OR HTRA1 OR HTRA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA 'Oka C., Some A., Kanda H., Kawachi M.;

RT "The role of murine serine protease HTRA in osteogenesis."?
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Protease that regulate the availability of IGFs by
 CC cleaving IGF-binding proteins (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (by similarity).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C; ALSO KNOWN AS THE
 CC DSGP/DEGP/DEGS FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IGFBP DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 KAZAL-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF172994; AAD49422.1; -.
 DR MGD: MGI:1929076; Pss11.
 DR InterPro: IPR000867; IGFBP.
 DR InterPro: IPR001478; PDZ.
 DR InterPro: IPR001940; Protease2C.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR002350; kazal.
 DR Pfam: PF00219; IGFBP; 1.
 DR Pfam: PF00050; kazal; 1.
 DR Pfam: PF00059; PDZ; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR Pfam: PF00834; PROTEASES2C.
 DR SMART: SM00121; IB; 1.
 DR SMART: SM00280; KAZAL; 1.
 DR SMART: SM00288; PDZ; 1.
 DR PROSITE: PS50106; PDZ; 1.
 KW Hydrolase; Serine protease; Growth factor binding; signal.

FT SIGNAL 1 22
 FT CHAIN 23 480
 FT DOMAIN 37 94
 FT DOMAIN 101 155
 FT DOMAIN 204 364
 FT DOMAIN 365 467
 FT ACT_SITE 220 220
 FT ACT_SITE 250 250
 FT ACT_SITE 328 328
 FT SEQUENCE 480 AA: 51246 MW: 54BB9BA6C99A7BF4 CRC64:
 Query Match
 Best Local Similarity 6.7%; Score 81; DB 1; Length 480;
 Matches 48; Conservative 26; Mismatches 73; Indels 72; Gaps 11;
 DB 16 GDAXXTMGACGYGNLYSGYGLTALSTALPFDGLSGACXELMCVNDPOMCKIGRSI 75
 DB 73 GAACGLOGPCGEGBLQCVLPGVASATVRRRAQGLCYCASSEPVCGSDAK----- 124
 QY 76 VVTATNFC-----PP-----GGAC-----DPN---HHFDLSQPTYEKIA-- 107
 DB 125 --TYTNLCOLRAASRRSEKILPPQPVIVLORACGCGEDPNSLRHKYNTADVVEFAFD 182
 QY 108 -----LYSGIIPVYRRVRCRKGSGIRFTINGHSYENLVLTNVGAGADVHSVSMKGSR 162
 DB 183 VYKHELK--LPESKRVVPAASGGLYSIDG-----LIVTN-----AHVTK-NR 227
 QY 163 TKQMLSRNMGONNSYLNQSLSPVYTTSDRRSVS 201
 DB 228 VKVELK-----NCATYEALIKDVDEKADIA 252

RESULT 13
 ID CYPH_BLAGE STANDARD: PRT: 164 AA.
 AC P54985;
 DT 01-OCT-1996 (Rel. 34, Created)

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CC EMBL: AI133035; CAB37075.1; -
 DR EMBL: AE001585; AAD18163.1; -
 DR EMBL: AE002237; AAF38570.1; -
 DR EMBL: AE002545; BAA98215.1; -
 DR TIGR: CP0770; -
 DR InterPro: IPR003368; DUF145.
 DR InterPro: IPR003357; OMP.
 DR Pfam: PF02415; DUF145; 1.
 DR Pfam: PF02385; OMP; 1.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 922 PROBABLE OUTER MEMBRANE PROTEIN PMPL.
 FT CONFLICT 14 14 F -> L (IN REF. 1).
 FT CONFLICT 375 375 Y -> C (IN REF. 1).
 FT CONFLICT 606 606 D -> N (IN REF. 1).
 FT SEQUENCE 922 AA; 100457 MW; DFF2AB633AB031C CRC64;
 SQ
 Query Match 7.0%; Score 84.5; DB 1; Length 922;
 Best Local Similarity 24.2%; Pred. No. 2.4;
 Matches 59; Conservative 29; Mismatches 81; Indels 75; Gaps 15;
 QY 6 INAAHFFXXGDAXXTMGAGCYGLYSOG-----YGL--ETAAALSTALPDQGLSCG 55
 DB 206 VNAQAIRFRAONTAKNGSSGA-----LYSDGDIDIDONAYVLFRENEALLTAIGKGAVC- 259
 QY 56 ACXELMCVNDPOWCIKRSIVVATNFCPPGACDP--PNHFF-DLSQPIYEKIALYKSGT 113
 DB 260 -----CL-----PTSGSTFPVPIYTFSDNKLVEERHNSIMGG- 292
 QY 114 IPVWYRVRCKRRSGGIRTINGHYFNLVLTNVGA-----GDVH-----SVSMKGS 161
 DB 293 -GAIYARLSTISSGPTLFNNISYAN---SONIGAIADITGGEISLSAEKGTITFGQ 348
 QY 162 RTKQMLSRNMGWQNSNYL-----NGOSLSF---VYTSDRKRSYSEFVAPPTYSFGQ 213
 DB 349 RTSLPFL-NGIHLQNAKFLQARNGYSIEFYDPTTSEADSGTQNLNGDKR---NK 402
 QY 214 TYTG 217
 DB 403 EYTG 406
 RESULT 11
 CATE_HUMAN
 ID CATE_HUMAN STANDARD: PRT; 339 AA.
 AC P07858;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cathepsin B precursor (EC 3.4.22.1) (Cathepsin B1) (APP secretase).
 GN CTSB OR CTSB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87017021; PubMed=3463996;
 RA Chan S.-J., San Segundo B., McCormick M.B., Steiner D.F.;
 RT "Nucleotide and predicted amino acid sequences of cloned human and
 mouse preprocathepsin B cDNAs.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:7721-7725(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=gastric carcinoma;
 RX MEDLINE=94156194; PubMed=8112600;
 RA Cao L., Taggart R.T., Berguin I.M., Moln K., Fong D., Sloane B.F.;
 RT "Human gastric adenocarcinoma cathepsin B: isolation and sequencing
 of full-length cDNAs and polymorphisms of the gene.";
 RL Gene 139:163-169(1994).
 RN [3]

RP SEQUENCE OF 80-126 AND 129-333.
 RC TISSUE=Liver;
 RX MEDLINE=85127484; PubMed=3972105;
 RA Ritonja A., Popovic T., Turk V., Wiedenmann K., Machleidt W.;
 RT "Amino acid sequence of human liver cathepsin B.";
 RL FEBS Lett. 181:169-172(1985).
 RN [4]
 RP SEQUENCE OF 131-339 FROM N.A.
 RX MEDLINE=86206063; PubMed=3010323;
 RA Fong D., Calhoun D.H., Hsieh W.-T., Lee B., Wells R.D.;
 RT "Isolation of a cDNA clone for the human lysosomal proteinase
 cathepsin B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2909-2913(1986).
 RN [5]
 RP SEQUENCE OF 80-91 AND 129-139.
 RC TISSUE=Liver;
 RX MEDLINE=92344620; PubMed=1637335;
 RA Moln K., Day N.A., Sameni M., Hasnain S., Hiram T., Sloane B.F.;
 RT "Human tumour cathepsin B. Comparison with normal liver cathepsin B.";
 RL Biochem. J. 285:427-434(1992).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
 RX MEDLINE=91330854; PubMed=1868826;
 RA Husli D., Zucic D., Turk D., Engh R.A., Mayr I., Huber R., Popovic T.,
 RT Turk V., Towatari T., Katunuma N., Bode W.;
 RT "The refined 2.15 A x-ray crystal structure of human liver cathepsin
 B: the structural basis for its specificity.";
 RL EMBO J. 10:2321-2330(1991).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
 RX MEDLINE=96197789; PubMed=8617353;
 RA Turk D., Podobnik M., Kuhnelt R., Dollner M., Turk V.;
 RT "Crystal structures of human procathepsin B at 3.2- and 3.3-A
 resolution reveal an interaction motif between a papain-like cysteine
 protease and its propeptide.";
 RL FEBS Lett. 384:211-214(1996).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=97446326; PubMed=9299326;
 RA Podobnik M., Kuhnelt R., Turk V., Turk D.;
 RT "Crystal structure of the wild-type human procathepsin B at 2.5-A
 resolution reveals the native active site of a papain-like cysteine
 protease zymogen.";
 RL J. Mol. Biol. 271:774-788(1997).
 RN [9]
 RP FUNCTION: THIOL PROTEASE WHICH IS BELIEVED TO PARTICIPATE IN
 INTRACELLULAR DEGRADATION AND TURNOVER OF PROTEINS. HAS ALSO
 BEEN IMPLICATED IN TUMOR INVASION AND METASTASIS.
 CC CATALYTIC ACTIVITY: HYDROLASES PROTEINS, WITH A SPECIFICITY
 RESEMBLING THAT OF PAPAIN.
 CC SUBUNIT: DIMER OF A HEAVY CHAIN AND A LIGHT CHAIN CROSS-LINKED
 BY A DISULFIDE BOND.
 CC SUBCELLULAR LOCATION: Lysosomal.
 CC SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 PAPAIN FAMILY OF THIOL PROTEASES.
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DR EMBL: M14221; AAA52129.1; -
 DR EMBL: L16510; AAC37547.1; -
 DR EMBL: M13230; AAA52125.1; -
 DR PIR: A26496; KHHOB.
 DR PIR: A25432; A25432.
 DR PIR: S16513; S16513.
 DR PIR: S16514; S16514.
 DR PDB: 1HUC; 26-JAN-95.
 DR PDB: 1CSB; 03-APR-96.
 DR PDB: 1PBH; 23-FEB-98.


```

RESULT 7
MP21_MAZE
ID MP21_MAZE STANDARD; PRT; 191 AA.
AC 007154;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Pollen allergen Zea m 1 (Zea m 1).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Penicillidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RX MEDLINE=94010312; PubMed=8406014;
RA Broadwater A.H., Rubinstein A.L., Chay C.H., Klapper D.G.,
RA Bedinger P.A.;
RT "Zea m1, the maize homolog of the allergen-encoding Lol p1 gene of
RT rye grass.";
RL Gene 131:227-230(1993).
CC -1- TISSUE SPECIFICITY: POLLEN TISSUE.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION LOW BEFORE AND HIGH AFTER
CC POLLEN MITOSIS.
CC -1- DISEASE: CAUSES MAIZE POLLEN ALLERGY.
CC -1- SIMILARITY: BELONGS TO THE LOL P 1 FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
CC -----
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CC -----
CC EMBL; L14271; AAA33496.1; -
CC PIR; JC1524; JC1524.
CC HSSP; P43214; IMHO.
CC MAZEDB; 65840; -
CC InterPro: IPR000882; Pollen_allergen.
CC Pfam: PF01357; Pollen_allergen.1.
CC PRINTS; PRO1225; EXPANSINFAMILY.
CC ProDom; PD002179; Pollen_allergen.1.
CC DR PROSITE; PS50843; EXPANSIN_CBD.1.
CC DR PROSITE; PS50842; EXPANSIN_EG45.1.
CC Allergen; Multigene family.
CC FT DOMAIN 1 EXPANSIN-LIKE EG45.
CC FT DOMAIN 105 186 EXPANSIN-LIKE CBD.
CC SEQUNCE 191 AA; 21362 MW; 6E2A9DE921C45C63 CRC64;

Query Match 14.8%; Score 178; DB 1; Length 191;
Best Local Similarity 27.0%; Pred. No. 5.1e-10;
Matches 53; Conservative 33; Mismatches 88; Indels 22; Gaps 7;

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Db 175 PANMRPDVYTSNVGF 190

RESULT 8
ID GUN5_TRIRE STANDARD; PRT; 242 AA.
AC P43317;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)
DE (Cellulase V) (EG V).
GN Egl5.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=QM9414 / RUT C-30;
RX MEDLINE=95075308; PubMed=7984103;
RA Saloheimo A., Henriksas B., Holten A.-M., Telemann O., Penttilae M.;
RT "A novel, small endoglucanase gene, egl5, from Trichoderma reesei
RT isolated by expression in yeast.";
RL Mol. Microbiol. 13:219-228(1994).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILLY K (FAMILY 45 OF GLYCOSYL
CC HYDROLASES).
CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
CC -----
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CC -----
CC EMBL; Z3381; CAAB3846.1; -
CC HSSP; P00725; 2CBH.
CC InterPro: IPR000254; CBD_fungal.
CC DR PROSITE; PS001821; CBD_fungal.1.
CC Pfam; PF00734; CBD_1.1.
CC DR Pfam; PF02015; Glyco_hydro_45.1.
CC ProDom; PD001821; CBD_fungal.1.
CC DR SMART; SM00236; FCBD.1.
CC DR PROSITE; PS00562; CBD_FUNGAL.1.
CC DR PROSITE; PS50842; EXPANSIN_EG45.1.
CC DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45.1.
CC Cellulose degradation; Hydrolase; Glycosidase; Signal.
CC FT SIGNAL 1 17 POTENTIAL.
CC FT CHAIN 18 242 ENDOGLUCANASE V.
CC FT ACT_SITE 27 27 NUCLEOPHILE (BY SIMILARITY).
CC FT ACT_SITE 134 134 PROTON DONOR (BY SIMILARITY).
CC FT DOMAIN 18 182 CATALYTIC.
CC FT DOMAIN 183 205 PRO/SER-RICH (LINKER).
CC FT CARBOHYD 206 242 CELLULOSE-BINDING (BY SIMILARITY).
CC FT DOMAIND 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT DISULFID 213 230 BY SIMILARITY.
CC FT DISULFID 224 240 BY SIMILARITY.
CC SEQUNCE 242 AA; 24411 MW; CC033FC51326C71D CRC64;

Query Match 9.0%; Score 108.5; DB 1; Length 242;
Best Local Similarity 30.6%; Pred. No. 0.0028;
Matches 37; Conservative 9; Mismatches 40; Indels 35; Gaps 5;

```

OS Phalaris aquatica (Canary grass).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 CC Poaceae; Phalaris.
 OX NCBI_TaxID=28479;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-Pollen;
 RX MEDLINE=96105569; Pubmed=8564724;
 RA Suphloglu C., Singh M.B.;
 RT "Cloning, sequencing and expression in Escherichia coli of Pha a 1
 RT and four isoforms of Pha a 5, the major allergens of canary grass
 RT pollen."; Allergy 25:853-865(1995).
 RL Clin. Exp. Allergy 25:853-865(1995).
 RN [2]
 RP SEQUENCE OF 30-49.
 RX MEDLINE=93319091; Pubmed=7687099;
 RA Suphloglu C., Singh M.B., Simpson R.J., Ward L., Knox R.B.;
 RT "Identification of canary grass (Phalaris aquatica) pollen allergens
 RT by immunoblotting: IgE and IgG antibody-binding studies.";
 RL Allergy 48:273-281(1993).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
 CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 CC -----
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 CC -----
 DR EMBL: S80654; AAB35984.1; -
 DR HSSP: P43214; IMHO.
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PROSITE: PD002179; Pollen_allergen; 1.
 DR PROSITE: PS50843; EXPANSIN_CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 KW Allergen; Glycoprotein; Signal.
 FT CHAIN 1 29
 FT DOMAIN 67 173 MAJOR POLLEN ALLERGEN PHA A 1.
 FT DOMAIN 187 268 EXPANSIN-LIKE EG45.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 37 37 P -> G (IN REF. 2).
 SQ SEQUENCE 269 AA; 29011 MW; 05835A58ACE877F CRC64;
 Query Match 16.8%; Score 202.5; DB 1; Length 269;
 Best Local Similarity 28.5%; Pred. No. 3,4e-12;
 Matches 65; Conservative 36; Mismatches 90; Indels 37; Gaps 11;
 Oy 5 WTNAAHAFYX--XDAAXXTMGACGYNLSQGYGLTALSTALFDGSLGCAEXELMC 62
 Db 47 WLDKSTWYMGKPTGAGPKDNGAGCYKDVKAPFNGMTGCGNTPIFKDGSGCSCEFLKC 106
 Oy 63 VNDPWCICKGRSIVVTAATN-----FCPPGGACDPRNHHFDSQPIYKIA-----LYK 110
 Db 107 -SKPESC-SGEPITVHTDDNEPIAP-----YHFDLSGHAFSGSMKKKEEENVRG 155
 Oy 111 SGIIPIVYRVRVRCRSGGIRFTIN---GHSYFNLYLVTVNGAGDVHYSVM-KSRTKW 165
 Db 156 AGELELGFRRVKKCKYPGDTKPTFIVEKGSNPNYLLLVKVVDDGDDVVAADIKKCKDKW 215
 Oy 166 QLMRRNMGQNNQNS--YLNQGSLSFYV--TSDRSKSVSPFNNAAPPW 209
 Db 216 IELKESWGAIMRIDTPKLTG--PFTVRYTTEGTAKEEDVAPFGW 260

RESULT 6
 ID MPOL_ORYSA
 AC 040638;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Major pollen allergen Ory s 1 precursor (Ory s 1).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Anther;
 RX MEDLINE=96069591; Pubmed=7590339;
 RA Xu H., Theerakulpisut P., Gouding N., Suphloglu C., Singh M.B.,
 RA Bhalla P.L.;
 RT "Cloning, expression and immunological characterization of Ory s 1,
 RT the major allergen of rice pollen.";
 RL Gene 164:255-259(1995).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MATURE ANTHERS BUT NOT IN
 CC VEGETATIVE OR OTHER FLORAL TISSUES.
 CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
 CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U31771; AAB6533.1; -
 DR HSSP: P43214; IMHO.
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PROSITE: PD002179; Pollen_allergen; 1.
 DR PROSITE: PS50843; EXPANSIN_CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 KW Allergen; Glycoprotein; Signal; Multigene family.
 FT CHAIN 1 23
 FT DOMAIN 61 164 MAJOR POLLEN ALLERGEN ORY S 1.
 FT DOMAIN 178 259 EXPANSIN-LIKE EG45.
 FT CARBOHYD 32 32 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 263 AA; 28497 MW; B1C5F24EA398DD60 CRC64;
 Query Match 15.7%; Score 188.5; DB 1; Length 263;
 Best Local Similarity 31.3%; Pred. No. 7.2e-11;
 Matches 63; Conservative 29; Mismatches 82; Indels 27; Gaps 11;
 Oy 23 GGACGYNLSQGY--GLETAALSTALFDGSLGCAEXELMCVNDPWCIC-KRSIVVYAT 80
 Db 61 GGACGYKVDKAPFLGAMNSCG--NDPFLFKDGKCGSGCFELKC-SKPEACSDKALIHVTD 118
 Oy 81 NCPGPGACDPR--NHFDLSQPIYKIA-----LYKSGIIPIVYRVRVRCRSGGIRFTIN 134
 Db 119 N-----DEPIAAVNHFDLSGLAMAKDKGDELRKAGIIDPFRVKKYPADYKIRFPH 170
 Oy 135 ----GHSYFNLYLVTVNGAGDVHYSVM--KSRTKQMLMSNMGQNNQNS--YLNQGS 186
 Db 171 IEKASPNYLLLVKVVADGDVVEVEIKEGSE-EMWALKESWGAIMRIDTPKPIKGP 229
 Oy 187 LSFVYTTSDRSKSVSPFNNAAPP 207
 Db 230 SVRYTTEGARSSAEDAIIDP 250

RESULT 2			
MPCL_CYNDA			
ID	MPCL_CYNDA	STANDARD;	PRT; 246 AA.
AC	004701;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Major pollen allergen Cyn d 1.		
GN	CYNDA1.		
OS	Cynodon dactylon (Bermuda grass).		
OC	Eukaryote: Viridiplantae: streps.		
OC	Spermatophyta: Magnoliophyta: Embryophyta; Tracheophyta;		
OC	Chloridoideae: Magnoliophyta: Liliopsida: Poales; Poaceae; PACC clade		
OC	NCBI_TaxID=28909;		
ON			

MPC1_CYN

Accession	Protein	Length (aa)	Weight (kDa)	PI	Source	Notes
DR EMBL: S83343; AAB50734.2; -	EMBL	39	145		EXPANSIN-LIKE EC45.	
DR HSSP: P43214; 1WHO.	HSSP	159	240		EXPANSIN-LIKE CBD.	
DR InterPro: IPR000882; Pollen_allergen.	InterPro	9			N-LINKED (GLCNAC. .) (POTENTIAL).	
DR Pfam: PF01357; Pollen_allergen.1.	Pfam					
DR PRINTS: PRO1225; EXPANSINFAMILY.	PRINTS					
DR ProDom: PD002179; Pollen_allergen.1.	ProDom					
DR PROSITE: PS50843; EXPANSIN_CBD.1.	PROSITE					
DR PROSITE: PS50842; EXPANSIN_EC45; 1.	PROSITE					
KW Allergen.	KW					
FT DOMAIN	FT	39	145		EXPANSIN-LIKE EC45.	
FT DOMAIN	FT	159	240		EXPANSIN-LIKE CBD.	
FT CARBOHYD	FT	9			N-LINKED (GLCNAC. .) (POTENTIAL).	
SEQUENCE	SEQUENCE	246 AA:	2688 MW:	43D8442DBA589322	CR664;	

RESULT 3			
MPIL_LOLPR			
ID	MPIL_LOLPR	STANDARD:	PRT: 263 AA.
AC	P14946;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-AUG-1991 (Rel. 19, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	PolLEN allergen Lol p 1 precursor (Lol p 1) (Allergen R7).		
OS	Lolium perenne (Perennial ryegrass).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;		
OC	Poaceae; Lolium.		
OX	NCBI_LTaxID=45522;		

MPL1_LOLPR

RP SEQUENCE OF 24-53.
RC TISSUE-POLLEN:
MEDLINE=86242068; PubMed=3718469;
RX Cottle G.P., Moran D.M., Standaert R.;
RT "Photochemical and immunochemical characterization of allergenic
RT proteins from ryegrass (Lolium perenne) pollen prepared by a rapid
RT and efficient purification method.";
RJ Biochem. J. 234:305-310(1986).
M

RN SEQUENCE OF 236-263.
 RP MEDLINE=89364850; Pubmed=2475768;
 RA Esch R.E., Klapper D.G.;
 RT "Isolation and characterization of a major cross-reactive grass group
 I allergenic determinant."
 RL Mol. Immunol. 26:557-561(1989).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
 CC -1- SIMILARITY: BELONGS TO THE LOL P 1 FAMILY OF ALLELGENS.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 CC -----
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:50:30 ; Search time 5.73432 Seconds
(without alignments)
1499.000 Million cell updates/sec

Title: US-09-896-301-3

Perfect score: 1204
Sequence: 1 HMGFWINAHATFYXXGDAXX.....NVAPPTMSFGQTYTGCGFRY 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217.5	18.1	263	1	MPPI_PHLPR
2	216	17.9	246	1	MPPI_PHLPR
3	215.5	17.9	263	1	MPPI_PHLPR
4	205.5	17.1	263	1	MPPI_PHLPR
5	202.5	16.8	263	1	MPPI_PHLPR
6	188.5	15.7	263	1	MPPI_PHLPR
7	178	14.8	191	1	MPPI_PHLPR
8	108.5	9.0	242	1	MPPI_PHLPR
9	92	7.6	333	1	MPPI_PHLPR
10	84.5	7.0	333	1	MPPI_PHLPR
11	84	7.0	339	1	MPPI_PHLPR
12	81	6.7	480	1	MPPI_PHLPR
13	79	6.6	164	1	MPPI_PHLPR
14	78	6.5	649	1	MPPI_PHLPR
15	78	6.5	1553	1	MPPI_PHLPR
16	77.5	6.4	377	1	MPPI_PHLPR
17	77	6.4	1115	1	MPPI_PHLPR
18	77	6.4	1403	1	MPPI_PHLPR
19	77	6.4	1451	1	MPPI_PHLPR
20	76.5	6.4	305	1	MPPI_PHLPR
21	76.5	6.4	305	1	MPPI_PHLPR
22	76.5	6.4	335	1	MPPI_PHLPR
23	76.5	6.4	340	1	MPPI_PHLPR
24	76	6.3	491	1	MPPI_PHLPR
25	75.5	6.3	213	1	MPPI_PHLPR
26	75	6.2	376	1	MPPI_PHLPR
27	75	6.2	1038	1	MPPI_PHLPR
28	74.5	6.2	504	1	MPPI_PHLPR
29	74.5	6.2	546	1	MPPI_PHLPR
30	74	6.1	493	1	MPPI_PHLPR
31	74	6.1	526	1	MPPI_PHLPR
32	73.5	6.1	340	1	MPPI_PHLPR
33	73.5	6.1	363	1	MPPI_PHLPR

34	73.5	6.1	491	1	TYTR_LEIDO
35	73.5	6.1	1246	1	TYTR_LEIDO
36	73	6.1	1038	1	TYTR_LEIDO
37	73	6.1	2491	1	TYTR_LEIDO
38	73	6.1	3010	1	TYTR_LEIDO
39	72.5	6.0	480	1	TYTR_LEIDO
40	72.5	6.0	1004	1	TYTR_LEIDO
41	72.5	6.0	319	1	TYTR_LEIDO
42	71.5	5.9	308	1	TYTR_LEIDO
43	71.5	5.9	502	1	TYTR_LEIDO
44	71.5	5.9	561	1	TYTR_LEIDO
45	71.5	5.9	561	1	TYTR_LEIDO

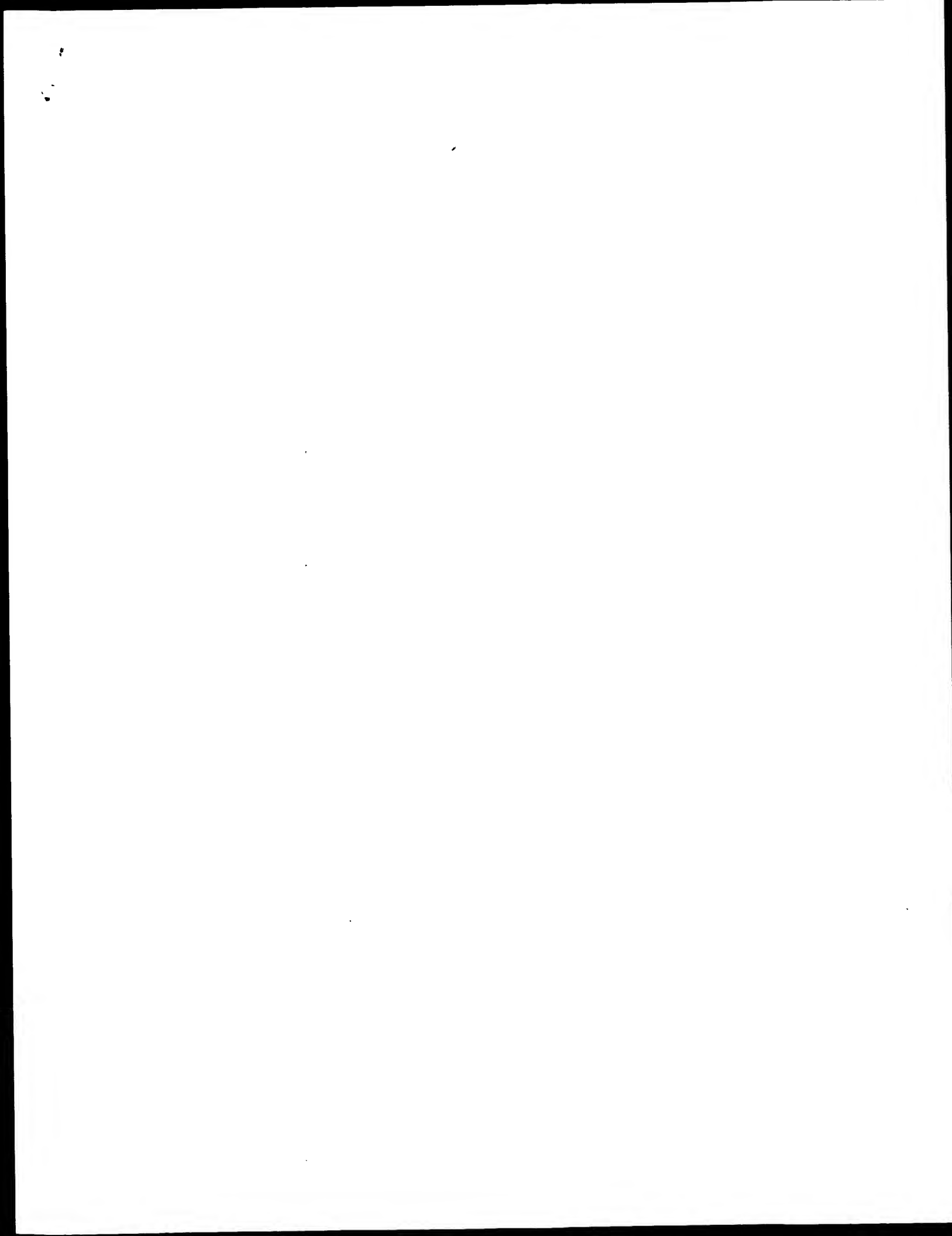
ALIGNMENTS

RESULT 1
MPPI_PHLPR STANDARD: PRT: 263 AA.
ID MPPI_PHLPR
AC P43213
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Pollen allergen Phl p 1 precursor (Phl p 1).
GN PHLP.
OS Phleum pratense (Common timothy).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Poaceae; Phleum.
OX NCBI_TaxID=15957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=polle;
RX MEDLINE=95015525; PubMed=7930302;
RA Laffer S., Valente R., Vitale S., Susani M., van Ree R., Kraft D.,
RA Scheiner O., Duchene M.;
RT *Complementary DNA cloning of the major allergen Phl p 1 from timothy
RT grass (Phleum pratense); recombinant Phl p 1 inhibits IgE binding to
RT group 1 allergens from eight different grass species.";
RT
RL J. Allergy Clin. Immunol. 94:689-698(1994).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE LIL P 1 FAMILY OF ALLERGENS.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.

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EMBL: X78813; CAA55390.1; -
DR HSSP: P43214; IMHO.
DR InterPro: IPRO00882; Pollen-allergen.
DR Pfam: PF01357; Pollen.allergen; 1.
DR PRINTS: PR01225; EXPANSIN-FAMILY.
DR ProDom: PD002179; Pollen.allergen; 1.
DR PROSITE: PS50843; EXPANSIN-CBD; 1.
DR PROSITE: PS50842; EXPANSIN-EG45; 1.
KW Allergen; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 263 POLLEN ALLERGEN PHL P 1.
FT DOMAIN 61 167 EXPANSIN-LIKE EG45.
FT DOMAIN 181 262 EXPANSIN-LIKE CBD.
FT CARBOHYD 32 32 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 263 AA: 28457 MW: 0468249C17BC048 CRC64;

Query Match 18.1%; Score 217.5; DB 1; Length 263;
Best Local Similarity 28.2%; Pred. No. 1.2e-13;
Matches 66; Conservative 38; Mismatches 93; Indels 37; Gaps 11;



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Db      83  CYNQDPCWCLPG-STIVVATNECPNNALPNNAGGWCNPLQHPDLAOPVFOHTAQTKACI 141
OY      114  IPVYRRVRCRKGSGIFFTINGSHYFNLYLVTVNGAGDVHVSVMKGSRTKQMLSRNMG 173
Db      142  VPVAYRRIPCNRRKGIRFTINGSHYFNLYLVTVNGAGDVHVSVMKGSRTKQMLSRNMG 201
OY      174  QNMOSNYLNGOSLSFVVTSDRRSVSVFVAPPTWSFGOTY-TGGOF 220
Db      202  QNMGNANLNGOSLSFVVTSDGRTIVANNVASAGMSFGOTYATGAOF 249

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RESULT 15

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O9FUM3      PRELIMINARY:      PRT:      254 AA.
ID  O9FUM3
AC  O9FUM3:
DT  01-MAR-2001 (TREMBLrel. 16, Created)
DT  01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE  EXPANSIN 1.
GN  EXP1 OR EXP2.
OS  Prunus avium (Cherry), and
OC  Prunus cerasus.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX  NCBI_TaxID=42229, 140311;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  SPECIES=P. avium;
RA  Wu Z., Wiersma P.A.;
RT  "Differential Expression of Expansin Genes Isolated from Sweet Cherry
RL  (Prunus avium L.) During Fruit Ripening.";
RN  Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP  SEQUENCE FROM N.A.
RC  SPECIES=P. cerasus; TISSUE=RIPENING FRUIT;
RA  Yoo S.-D., Gao Z., Cantini C., Loeschner W., van Nocker S.;
RT  "Coordinated expression of genes encoding expansins and other cell
RT  wall-modifying enzymes is associated with pectin-related changes in
RT  the cell wall during ripening of cherry (P. cerasus) fruit.";
RL  Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF297521; AAG13982.1; -
DR  EMBL; AF350937; AAK48846.1; -
DR  InterPro: IPR000882; Pollen_allergen.
DR  Pfam: PF01357; Pollen_allergen; 1.
DR  PRINTS: PR01225; EXPANSINFAMILY.
DR  Prodom: PD002179; Pollen_allergen; 1.
SQ  SEQUENCE 254 AA; 27278 MW; 953A7EB2491FD0E1 CRC64;

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Query Match      73.9%; Score 889.5; DB 10; Length 254;
Best Local Similarity 71.2%; Pred. No. 3.2e-82;
Matches 161; Conservative 23; Mismatches 33; Indels 9; Gaps 2;

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OY      3  GPWIAHATFFXXGDAXXTMGACGYGMLYSQSGLETALSTALFPDGLSCGACXELMC 62
Db      30  GMEGCAHATFFYGGDASTMGACGYGMLYSQSGLETALSTALFPDGLSCGACXELMC 89
OY      63  VNDPQWCIKGRSIVTATNECP-----GCACDPNHHFPLDSCPIYEKIALYKSGIT 114
Db      90  NNDRPWCPRG-SIVTATNECPNFAQSNNDGWCNPLQHPDLAEPALQIAYRAGIV 148
OY      115  PVMTRRVACRKGSGIRFTINGSHYFNLYLVTVNGAGDVHVSVMKGSRTKQMLSRNMG 174
Db      149  PVTRRVACRKGSGIRFTINGSHYFNLYLVTVNGAGDVHVSVMKGSRTKQMLSRNMG 208
OY      175  QNMOSNYLNGOSLSFVVTSDRRSVSVFVAPPTWSFGOTY-TGGOF 220
Db      209  QNMGNANLNGOSLSFVVTSDGRTIVANNVASAGMSFGOTYATGAOF 254

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Search completed: October 11, 2002, 14:59:40
 Job time : 20.169 secs

RT "Genomic sequence for Arabidopsis thaliana BAC T24P13 from chromosome
 1."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN (5)
 RP SEQUENCE FROM N.A.
 RA Chouk R., Shann P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 Khan S., Kim C., Altafi H., Bel B., Chin C., Chlou J., Choi E.,
 Conn L., Conway A., Gonzalez A., Hansen N., Howling B., Koo T., Lam B.,
 Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharzky N.,
 Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 Thavert A., Tortum M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 Theologis A., Ecker J.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN (6)
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA Cho H., Cosgrove D.J.;
 RT "Expansin AEXPT0 affects organ growth and morphology in Arabidopsis
 thaliana."
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN (7)
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA Durachko D.M., Sheerthan T.Y., Cosgrove D.J.;
 RT "AEXPT0 is expressed in the trichomes, petioles, midribs, and pedicel
 abscission zone."
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN (8)
 RP EMBL; AC006535; AAF87031.1; -;
 DR EMBL; AF229437; AAF61712.1; -;
 DR EMBL; AF229431; AAF61713.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PRO1225; EXPANSNFAMLY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 DR PROSITE: 249 AA; 26428 MW; 63D014410D4ABBA1 CRC64;
 SQ SEQUENCE 249 AA; 26428 MW; 63D014410D4ABBA1 CRC64;
 Query Match 77.0%; Score 927.5; DB 10; Length 249;
 Best Local Similarity 73.6%; Pred. No. 4,3e-86;
 Matches 167; Conservative 22; Mismatches 29; Indels 9; Gaps 2;
 QY 3 GPMINAHATFYXXDXXTMGACGCGNLYSGYGLFETALSTALFDGGLSCGACXELMC 62
 DB 24 GPMINAHATFYXXDXXTMGACGCGNLYSGYGLFETALSTALFDGGLSCGACXELMC 62
 QY 63 VNDPQMCIRGSIIVTATNFCPP-----GGACDPNNHFDLSQPIYEXIALYKSGII 114
 DB 84 EMDGKWCPLG-SIVVTATNFCPPNNALANNNGWCNPPLEHFDLAQVFORIAQYRAGIV 142
 QY 115 PVMYRRVRCRSGIRFTINGSHYFNLVYTVNGAGDVHVSVMKSGRTKQMLSRNMGQ 174
 DB 143 PVMYRRVRCRSGIRFTINGSHYFNLVYTVNGAGDVHVSVMKSGRTKQMLSRNMGQ 174
 QY 175 NMOSNSYLNQGLSLFVVTSDRRSVSFNVPPTMSFGQTYGGQFR 221
 DB 203 NMOSNSYLNQGLSLFVVTSDRRSVSFNVPPTMSFGQTYGGQFR 221
 RESULT 8
 Q38863 PRELIMINARY; PRT; 237 AA.
 AC Q38863;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE EXPANSIN AT-EXPI (FRAGMENT).
 GN AT-EXPI.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96016146; PubMed=7568110;
 RA Sheerthan T.Y., Shi J., Durachko D.M., Gullitman M.J.,
 McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
 RT "Molecular cloning and sequence analysis of expansins--a highly
 conserved, multigene family of proteins that mediate cell wall
 extension in plants."
 RT Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
 RL EMBL; U30476; AAB38070.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PRO1225; EXPANSNFAMLY.
 DR Prodom: PD002179; Pollen_allergen; 1.
 FT NON_TER 1
 SQ SEQUENCE 237 AA; 25155 MW; 0E5A2C89C2943682 CRC64;
 Query Match 75.5%; Score 909.5; DB 10; Length 237;
 Best Local Similarity 73.1%; Pred. No. 2,7e-84;
 Matches 166; Conservative 19; Mismatches 33; Indels 9; Gaps 2;
 QY 3 GPMINAHATFYXXDXXTMGACGCGNLYSGYGLFETALSTALFDGGLSCGACXELMC 62
 DB 12 GPMINAHATFYXXDXXTMGACGCGNLYSGYGLFETALSTALFDGGLSCGACXELMC 62
 QY 63 VNDPQMCIRGSIIVTATNFCPP-----GGACDPNNHFDLSQPIYEXIALYKSGII 114
 DB 72 QNDGKWCPLG-SIVVTATNFCPPNNALPNNAGWCNPPQOHFDLSQPVFORIAQYRAGIV 130
 QY 115 PVMYRRVRCRSGIRFTINGSHYFNLVYTVNGAGDVHVSVMKSGRTKQMLSRNMGQ 174
 DB 131 PVMYRRVRCRSGIRFTINGSHYFNLVYTVNGAGDVHVSVMKSGRTKQMLSRNMGQ 174
 QY 175 NMOSNSYLNQGLSLFVVTSDRRSVSFNVPPTMSFGQTYGGQFR 221
 DB 191 NMOSNSYLNQGLSLFVVTSDRRSVSFNVPPTMSFGQTYGGQFR 221
 RESULT 9
 Q92P36 PRELIMINARY; PRT; 249 AA.
 AC Q92P36;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ALPHA-EXPANSIN PRECURSOR.
 GN NT-EXPA.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 NCBI_TaxID=4097;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, BY2;
 RX MEDLINE=99026292; PubMed=9808735;
 RA Link B.M., Cosgrove D.J.;
 RT "Acid-growth response and alpha-expansins in suspension cultures of
 bright yellow 2 tobacco."
 RL Plant Physiol. 118:907-916(1998).
 DR EMBL; AF049353; AAC96080.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PRO1225; EXPANSNFAMLY.

[illegible]

GOLD98			
ID	Q9LDR9	PRELIMINARY;	PRT; 249 AA.
AC	Q9LDR9;		
DT	01-OCT-2000	(TREMBLE1, 15, Created)	
DT	01-OCT-2000	(TREMBLE1, 15, Last sequence update)	
DT	01-DEC-2001	(TREMBLE1, 19, Last annotation update)	
DE	T24P13.15	(EXPANSIN 10).	
GN	Exp10.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Johnson-Hopson C., Dunn P., Brooks S., Buehler E., Chao O., Khan S.,		
RA	Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chou J., Choi E., Lam B.,		
RA	Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,		
RA	Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,		
RA	Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,		
RA	Theaverl A., Tortumt M., Vaysberg M., Yu G., Federspiel N.A.,		
RA	Theologis A., Ecker J.R.;		

DR Pfam; PF01357; Pollen_allergen: 1.
 DR PRINTS; PRO1225; EXPANSNFAMILY.
 DR Prodom; PD002179; Pollen_allergen: 1.
 SO SEQUENCE 255 AA; 27611 MW; 7580595A30DC414B CRC64;

Query Match 99.3%; Score 1195; DB 10; Length 255;
 Best Local Similarity 97.7%; Pred. No. 3.2e-113;
 Matches 217; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 HMGPIINAHATFYXXGDAAXXTMGACGYNLYSGYGLFETALSTALFDGSLGACACXEL 60
 |||||
 DB 34 HMGPIINAHATFYXXGDAAXXTMGACGYNLYSGYGLFETALSTALFDGSLGACACXEL 93
 |||||
 QY 61 MCVNDPQMCIRGSRIVATATNFCPPGACDPPNHHFELSOPRYEKIALYKSGIIPVWYR 120
 |||||
 DB 94 MCVNDPQMCIRGSRIVATATNFCPPGACDPPNHHFELSOPRYEKIALYKSGIIPVWYR 153
 |||||
 QY 121 VRCRSGGIRFTINGHSYFNLVLTNMGAGDVHSVSKSGRTKQMLSRMGMQMSNS 180
 |||||
 DB 154 VRCRSGGIRFTINGHSYFNLVLTNMGAGDVHSVSKSGRTKQMLSRMGMQMSNS 213
 |||||
 QY 181 YLNGSLSFVVTSDRSVSEFNAPPTWSEFGQTYTGQFR 222
 |||||
 DB 214 YLNGSLSFVVTSDRSVSEFNAPPTWSEFGQTYTGQFR 255
 |||||

RESULT 2

Q9FNT1 PRELIMINARY; PRT; 245 AA.

ID 09FNT1
 AC 09FNT1
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE EXPANSIN.
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
 NCBI_TaxID=3827;
 RX 11
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
 RA Doplco B., Sanchez M.A., Labrador E.;
 RT "An expansin is expressed in chickpea epicotyls."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ291816; CAC19183.1;
 DR InterPro; IPR000882; Pollen_allergen.
 DR PRINTS; PRO1225; EXPANSNFAMILY.
 DR Prodom; PD002179; Pollen_allergen: 1.
 SO SEQUENCE 245 AA; 26469 MW; 0E6BF0C35A38B23 CRC64;

Query Match 83.3%; Score 1003; DB 10; Length 245;
 Best Local Similarity 82.6%; Pred. No. 9.2e-94;
 Matches 180; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 5 WINAHATFYXXGDAAXXTMGACGYNLYSGYGLFETALSTALFDGSLGACACXELMCVN 64
 |||||
 DB 28 WINAHATFYXXGDAAXXTMGACGYNLYSGYGLFETALSTALFDGSLGACACXELMCVN 87
 |||||
 QY 65 DPMQICIRGSRIVATATNFCPPGACDPPNHHFELSOPRYEKIALYKSGIIPVWYR 124
 |||||
 DB 88 DPMQICIRGSRIVATATNFCPPGACDPPNHHFELSOPRYEKIALYKSGIIPVWYR 147
 |||||
 QY 125 RSGGIRFTINGHSYFNLVLTNMGAGDVHSVSKSGRTKQMLSRMGMQMSNSYLNG 184
 |||||
 DB 148 RSGGIRFTINGHSYFNLVLTNMGAGDVHSVSKSGRTKQMLSRMGMQMSNSYLNG 207
 |||||
 QY 185 QSLSFVVTSDRSVSEFNAPPTWSEFGQTYTGQFR 222
 |||||
 DB 208 QSLSFVVTSDRSVSEFNAPPTWSEFGQTYTGQFR 245
 |||||

RESULT 3

Q92P31 PRELIMINARY; PRT; 239 AA.

ID Q92P31
 AC Q92P31
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE EXPANSIN PRECURSOR.
 GN EXP5.
 OS Lycopersicon esculentum (Tomato).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 NCBI_TaxID=4081;
 RX 11
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV. 91347; TISSUE=FRUIT;
 RA MEDLINE=99178803; PubMed=10080718;
 RA Brumwell D.A., Harpster M.H., Dunsul P.;
 RT "Differential expression of expansin gene family members during growth
 and ripening of tomato fruit."
 RL Plant Mol. Biol. 39:161-169(1999).
 DR EMBL; AF059489; AAD13633.1;
 DR InterPro; IPR000882; Pollen_allergen.
 DR Pfam; PF01357; Pollen_allergen: 1.
 DR PRINTS; PRO1225; EXPANSNFAMILY.
 DR Prodom; PD002179; Pollen_allergen: 1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN.
 SQ SEQUENCE 239 AA; 25606 MW; 1C43BF3A1021788C CRC64;

Query Match 77.5%; Score 933.5; DB 10; Length 239;
 Best Local Similarity 77.2%; Pred. No. 1e-86;
 Matches 169; Conservative 20; Mismatches 29; Indels 1; Gaps 1;

QY 3 GPMINAHATFYXXGDAAXXTMGACGYNLYSGYGLFETALSTALFDGSLGACACXELMC 62
 |||||
 DB 22 GPMINAHATFYXXGDAAXXTMGACGYNLYSGYGLFETALSTALFDGSLGACACXELMC 81
 |||||
 QY 63 VNDPQMCIRGSRIVATATNFCPPGACDPPNHHFELSOPRYEKIALYKSGIIPVWYR 122
 |||||
 DB 82 VNDPQMCIRGSRIVATATNFCPPGACDPPNHHFELSOPRYEKIALYKSGIIPVWYR 140
 |||||
 QY 123 CRSGGIRFTINGHSYFNLVLTNMGAGDVHSVSKSGRTKQMLSRMGMQMSNSYL 182
 |||||
 DB 141 CRSGGIRFTINGHSYFNLVLTNMGAGDVHSVSKSGRTKQMLSRMGMQMSNSYL 200
 |||||
 QY 183 NGSLSFVVTSDRSVSEFNAPPTWSEFGQTYTGQFR 221
 |||||
 DB 201 NGSLSFVVTSDRSVSEFNAPPTWSEFGQTYTGQFR 239
 |||||

RESULT 4

Q9FUM2 PRELIMINARY; PRT; 252 AA.

ID Q9FUM2
 AC Q9FUM2
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE EXPANSIN 2.
 GN EXP2.
 OS Prunus avium (Cherry).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids I; Rosales; Rosaceae; Amygdaloidae; Prunus.
 NCBI_TaxID=42229;
 RX 11
 RN SEQUENCE FROM N.A.
 RA Wu Z., Wiersma P.A.;
 RT "Differential Expression of Expansin Genes Isolated from Sweet Cherry
 (Prunus avium L.) during Fruit Ripening";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF297522; AAG13983.1;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:51:00 : Search time 19.169 Seconds

(without alignments)
2003.488 Million cell updates/sec

Title: US-09-896-301-3

Perfect score: 1204

Sequence: 1 HMGWPNNAATFYXGDXAXX.....NVAPTWSPGQTYTGQFRY 222

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rhodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	99.3	255	10 038864	038864 arabidopsis
2	1003	83.3	245	10 09FNT1	09fnt1 cicer arlet
3	933.5	77.5	239	10 092P31	092p31 lycopersico
4	931.5	77.4	252	10 09FUM2	09fum2 prunus aviu
5	929.5	77.2	247	10 09M517	09m517 triphysaria
6	928	77.1	242	10 09LIB1	09lib1 zinnia eleg
7	927.5	77.0	249	10 09LDR9	09ldr9 arabidopsis
8	909.5	75.5	237	10 038863	038863 arabidopsis
9	909.5	75.5	249	10 092P36	092p36 nicotiana t
10	909.5	75.4	250	10 09C554	09c554 arabidopsis
11	907.5	75.4	248	10 080622	080622 arabidopsis
12	896.5	74.5	249	10 093XP1	093xp1 prunus cera
13	892.5	74.1	254	10 082093	082093 prunus arme
14	892	73.9	254	10 09M515	09m515 triphysaria
15	889.5	73.9	254	10 09FUM3	09fum3 prunus aviu
16	886.5	73.6	245	10 09LIB2	09lib2 zinnia eleg

17	874.5	72.6	260	10 09FNT0	09fnt0 cicer arlet
18	873.5	72.5	253	10 093XP2	093xp2 prunus cera
19	871.5	72.4	253	10 09SMT1	09smt1 fragaria an
20	871.5	72.4	255	10 09FMA0	09fma0 arabidopsis
21	870.5	72.3	232	10 093493	093493 pinus taeda
22	870.5	72.3	253	10 09SWY1	09swy1 pinus taeda
23	867	72.0	252	10 09FS30	09fs30 prunus pers
24	865	71.8	252	10 081133	081133 prunus arme
25	864.5	71.8	232	10 093495	093495 pinus taeda
26	863.5	71.7	232	10 093492	093492 pinus taeda
27	861.5	71.6	253	10 09SMD4	09smd4 tumex palus
28	857.5	71.2	250	10 093625	093625 cucumis sat
29	856.5	71.1	232	10 093494	093494 pinus taeda
30	856.5	71.1	250	10 09FV9	09fv9 lycopersico
31	855.5	71.1	262	10 080932	080932 arabidopsis
32	852.5	70.8	247	10 082625	082625 lycopersico
33	852.5	70.8	258	10 049194	049194 gossypium h
34	850.5	70.6	249	10 092P35	092p35 nicotiana t
35	845.5	70.2	258	10 09L29	09l29 arabidopsis
36	842	69.9	253	10 022874	022874 arabidopsis
37	832.5	69.1	257	10 048818	048818 arabidopsis
38	832.5	69.1	258	10 041043	041043 pism sativ
39	825.5	68.6	260	10 09M259	09m259 arabidopsis
40	825.5	68.6	276	10 094KT6	094kt6 zea mays (m
41	824	68.4	255	10 09FIC5	09fic5 arabidopsis
42	823	68.4	255	10 038866	038866 arabidopsis
43	820.5	68.1	251	10 094631	094631 oryza sativ
44	816.5	67.8	257	10 09XG16	09xg16 lycopersico
45	815.5	67.7	246	10 093442	093442 oryza sativ

ALIGNMENTS

RESULT 1

038864 PRELIMINARY: PRT; 255 AA.
ID 038864;
AC 038864;
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE EXPANSIN ATEX5 (EXPANSIN-LIKE PROTEIN).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016146; PubMed=7568110;
RA Shcherban T.Y., Shi J., Durachko D.M., Gullifan M.J.,
RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansin--a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.,
RN Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RX MEDLINE=20277480; PubMed=10819329;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. 1. Sequence
RT features of the regions of 4,504,864 bp covered by sixty pl and TAC
RT clones.";
RT DNA Res. 7:131-135(2000).
DR EMBL; U30478; AAB38071.1; -;
DR EMBL; AB025615; BAA95756.1; -;
DR InterPro; IPR000882; Pollen_allergen.

PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147303.
PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 16-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 29-SEP-1999; 99US-0156458.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.

PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 88.6%; Score 115; DB 21; Length 281;
Best Local Similarity 87.1%; Pred No. 17e-103;
Matches 196; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 4 GWVNAHATFYGGDASGTMGACGYGNLYSOGYGTNTALSTALFNNGISGACFEIRQ 63
Db |||||||
QY 64 NDKKWCIPGSTIVYTATNFCPPNNALPNNAGKWCNPPQOHFDLSQVYFORIAQYRAGIVPV 123
Db :|||
QY 117 SDGAWCIPGAIIVTATNFCPPNNALPNNAGKWCNPPHHDLSQVYFORIAQYRAGIVPV 176
Db :|||||
QY 124 AYRRVPCVRRGIRFTINGHSYFNVLITNVGAGDVHSAMYGSRGTQAMSRMGOMW 183
Db :|||||
QY 177 SYRRVPCMRGIRFTINGHSYFNVLITNVGAGDVHSAMYGSRGTQAMSRMGOMW 236
Db :|||||
QY 184 QSNVYLNQSLSPKVTSDQTIIVSNXANAGNSFCQFTGAHVR 228
Db |||:|||||
Db 237 QSNVYLNQSLSPKVTASDGRIVSNNTIAPASMSFCQFTGRQFR 281

Search completed: October 11, 2002, 14:56:41
job time : 27.2399 secs

PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161923.
PR 29-OCT-1999; 99US-0162142.

Query Match 88.6% Score 115; DB 21; Length 253;
Best Local Similarity 87.1% Pred. No. 1.4e-103;
Matches 196; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 4 GVNNAHATFYGGDASGTMGACGYNLYSQYGTNTALSTALEFNNGLSCGACFEIRCO 63
DB 29 GVNNAHATFYGGDASGTMGACGYNLYSQYGTNTALSTALEFNNGLSCGACFEIRCO 88
QY 64 NDGKCLGSLVVTATNCPNNAALPNNAAGCNCPOOHFPLSQPVQRIQYRAGIYVP 123
DB 89 SDGAWCLPGLIIVTATNCPNNAALPNNAAGCNCPOOHFPLSQPVQRIQYRAGIYVP 148
QY 124 AYRRVPCVRGIRFTINGHSYFNLVLTITNGAGDVHSAAVWKSRTGQWMSRNMGM 183
DB 149 SYRRVPCVRGIRFTINGHSYFNLVLTITNGAGDVHSAAVWKSRTGQWMSRNMGM 208
QY 184 QSNVYLCQSLSEFKVTSDDQITVSNNAAGWSPGOTFTGAHVR 228
DB 209 QSNVYLCQSLSEFKVTSDDQITVSNNAAGWSPGOTFTGAHVR 253

RESULT 15

AAG43341
ID AAG43341 standard; Protein: 281 AA.

AC AAG43341;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 54161.

KW Protein identification: signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0121860.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0123788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0128845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131448.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 22-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
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PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match
Best Local Similarity

88.6%; Score 1115; DB 21; Length 251;
87.1%; Pred. No. 1.4e-103;

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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
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PR 10-SEP-1999; 99US-0153070.
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PR 15-SEP-1999; 99US-0154018.
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PR 26-OCT-1999; 99US-0161602.
PR 28-OCT-1999; 99US-0161920.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
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Best Local Similarity 87.1%; Pred. No. 14e-103;
Matches 196; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

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DB 27 GWNAHATFYGGDASGTMGACGYNLYSQGYGTMTALSTALFLNNGLSCGACFEIRCO 86

QY 64 NDGKWCIPGSTIVTATNFCPPNNALPNNAGGKCNPPQOHFDLSQPVFORIAQYRACIVPV 123
DB 87 SDGAWCLPGAIIVTATNFCPPNNALPNNAGGKCNPLHHPDLSQPVFORIAQYRACIVPV 146
QY 124 AYRRVPCVRGRIFFETTINGHSYFNLYLITVWGAGDVHSAVYKGSRTGQAMSRNNQNN 183
DB 147 SYRRVPCVRGRIFFETTINGHSYFNLYLITVWGAGDVHSAVYKGSRTGQAMSRNNQNN 206
QY 184 QSNSTYNGQSLSPKVTSDQITVSNKXANANAGSFGQTFGAHVR 228
DB 207 QSNNTLNGQALSPKVTASDGRFTVSNNTIAPASMSFGQTFGRQFR 251
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ID AAG4343 standard; Protein; 251 AA.
AC AAG4343;
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54163.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 03-JUN-1999; 99US-0137528.


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Query Match 90.5%; Score 1139; DB 21; Length 280;
Best Local Similarity 89.0%; Pred. No. 6.5e-106;
Matches 202; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
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PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 28-SEP-1999; 99US-0156458.
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Query Match 90.5%; Score 1139; DB 21; Length 259;
Best Local Similarity 89.0%; Pred. No. 5.9e-106;
Matches 202; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
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DB 33 GGGWNAHATRYGGDASCTGACGACGYNLYSGYGTATLALSTALFNNGSCGACFEIR 92
OY 62 CONDKWCLPESIVYTATNFCPPNNAALPNNAGCNPPOOHFDLSOPFORIAQYRAGIV 121
DB 93 CENDCKWCLPESIVYTATNFCPPNNAALNNGGCMCNPLEHFDLAQYVFORIAQYRAGIV 152
OY 122 PVAYRVPDCAVRGIGRTITNGSHYFNVLITNVGAGDVHSAWVKSRTGQAMSRMGO 181
DB 153 PVSRYRVPDCAVRGIGRTITNGSHYFNVLITNVGAGDVHSAWVKSRTGQAMSRMGO 212
OY 182 NMQSNSTYLNQALSFKVTTSDDQITVSNKXANACHSPQOTFTCAHVR 228
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XX AC AAG51645;
XX AC AAG51645;
XX DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65568.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PE 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126284.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0128234.
XX 06-APR-1999; 99US-0128714.
XX 08-APR-1999; 99US-0129845.
XX 16-APR-1999; 99US-0130077.
XX 19-APR-1999; 99US-0130449.
XX 21-APR-1999; 99US-0130510.
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XX 28-APR-1999; 99US-0131449.
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AA51631
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AC AA51631.
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65549.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 05-MAR-1999; 99US-0123180.
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RESULT 8
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KW termination sequence.
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Db	23	GGGWNMAHATYTGCGDASGTMGACGCGNLYSQGTGTNTAALSTALFNNGLSGCACEIR <td>82</td>	82
QY	62	CONGCKMCLPGSIYVTATNFCPPNNALPPNNAAGWCNPFDOHFDLSPQVFORIAQYRGIV <td>121</td>	121
Db	83	CENGGCKMCLPGSIYVTATNFCPPNNALANNNGCNCNPLEHFDIAQVFORIAQYRGIV <td>142</td>	142
QY	122	PVAYRVPVCYRGGIIRFTINGSHSYFNLYLTITNVGAGDVSAAVYKGSRTGQAMSRMGO <td>181</td>	181
Db	143	PVSYRVPVCYRGGIIRFTINGSHSYFNLYLTITNVGAGDVSAAIKGSRTVWQAMSRMGO <td>202</td>	202
QY	182	NWQSNSTLNGQSLSEFKYTTSDGQITIVSNKXANAGWSFGQITFGAHR <td>228</td>	228
Db	203	NWQSNSTLNGQSLSEFKYTTSDGRTIVSFNNAAPAWMSYQGFAGQFR <td>249</td>	249

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DT 18-OCW-2000 (first entry)
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Qy	62	CONDKWCLPGSIYVTATNFCPPNNALPNNAGCMCNPOQHEPDSOPVFORIAOYRAGIV	121
Db	75	CENDKWCCLPGSIYVTATNFCPPNNALPNNAGCMCNPLEHPDLAOPVFORIAOYRAGIV	134
Qy	122	PVAYRRVPCVRRGGIRFTINGHSYENLVLTIVWGAGADVHSAMVKGSRITGMOAMSRNMGQ	181
Db	135	PVSYRRVPCVRRGGIRFTINGHSYENLVLTIVWGAGADVHSAAIKGSRITVQAMSRNMGQ	194
Qy	182	NMQNSYTLNGOSLSFKVTTSDGQTTIVSNKXANAAGSFGQTFEGAHVR	228
Db	195	NMQNSYTLNGALSPFKVTTSDGRTIVSFNAAPAGWSYQTFEGAGQFR	241

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18-OCT-2000 (first entry)
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KW
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Arabidopsis thaliana.
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EP1033405-A2.
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PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0152363.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 16-SEP-1999; 99US-0154079.
PR 20-SEP-1999; 99US-0154739.
PR 23-SEP-1999; 99US-0155139.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 14-OCT-1999; 99US-0159638.

PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160880.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 89.0%; Pred. No. 5,3e-106;
Matches 202; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

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DB 75 CENDGKMCLEPGSTIVTATNFCPPNNALPNNAGWCNPPLEHFDLQPVQRIARAGIV 134
QY 122 PVAYRRVPCVRRGIRFTINGHSYFNLVLTIVNGAGDVHSAVKSRTGQAMSRNMQ 181
DB 135 PVSYRRVPCVRRGIRFTINGHSYFNLVLTIVNGAGDVHSAIKSRTVQAMSRNMQ 194
QY 182 NMQSNSTYLNQGSLSFKVTTSDGOTIYSNNKXARAGNRFQTFPGAHYR 228
DB 195 NMQSNSTYLNQGSLSFKVTTSDGOTIYSNNKXARAGNRFQTFPGAHYR 241

RESULT 3
ID AAG51633 standard; Protein; 241 AA.
AC AAG51633;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65551.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay: genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN
XX
XX
PD 06-SEP-2000.
XX
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-MAR-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0123788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.

PT Expansin proteins which alter the mechanical strength of
PT polysaccharide(s) - useful in paper mfr. and recycling
PS Disclosure: page 30-31; 60pp; English.

XX Expansins are a novel class of proteins that catalyse the extension
CC of plant cell walls and the weakening of the hydrogen bonds in
CC cellulose. 2 Expansins (AAR94528 and AAR94529) have been identified in
CC rice and 3 in Arabidopsis (AAR94530-32). A cDNA clone (AAR13320)
CC coding for cucumber expansin 29 (AAR94537) has been obtd. Expansins
CC can be used e.g. in the mfr., de-linking and recycling of paper, in
CC the textile industry, to aid delignification processes, to alter gel
CC mechanical strength, etc.

XX Sequence 228 AA:

Query Match 99.8%; Score 1257; DB 17; Length 228;
Best Local Similarity 100.0%; Pred. No. 7.2e-118;
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DB 61 RCQNDGKWCLEPSIVVTATNFCPPNNALPNNAGWCNPPQHFDSLQPVFORIAQYRAGI 120
OY 121 VVAVARVPCVRCGRFTNGHSYFNVLITNVGAGGVHSAMVKGSRGTGQAMSRMNG 180
DB 121 VVAVARVPCVRCGRFTNGHSYFNVLITNVGAGGVHSAMVKGSRGTGQAMSRMNG 180
OY 181 QMWOSNYSYLNQSLSEFKVTTSDQTIIVSNXNAGMSFGQFTTGAHVR 228
DB 181 QMWOSNYSYLNQSLSEFKVTTSDQTIIVSNXNAGMSFGQFTTGAHVR 228

RESULT 2
AAG06546
ID AAG06546 standard; Protein; 241 AA.

XX AAG06546;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 3357.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

OS EPI033405-A2.

PN EPI033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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PR 28-APR-1999; 99US-0131449.
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PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
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PR 08-JUN-1999; 99US-0138094.
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PR 14-JUN-1999; 99US-0139119.
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PR 18-JUN-1999; 99US-0139454.
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PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140685.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142380.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
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PR 19-JUL-1999; 99US-0144331.
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PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:49:55 ; Search time 25.2399 Seconds
(without alignments)
1003.367 Million cell updates/sec

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Perfect score: 1259
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1139	90.5	249	21	AA60545
6	1139	90.5	249	21	AA61632
7	1139	90.5	249	21	AA65164
8	1139	90.5	259	21	AA60544
9	1139	90.5	259	21	AA63161
10	1139	90.5	280	21	AA65165
11	1115	88.6	251	21	AA623852

12	1115	88.6	251	21	AA643343	Arabidopsis thalia
13	1115	88.6	253	21	AA623851	Arabidopsis thalia
14	1115	88.6	253	21	AA643342	Arabidopsis thalia
15	1115	88.6	281	21	AA643341	Arabidopsis thalia
16	1115	88.6	282	21	AA623850	Arabidopsis thalia
17	1046	83.1	250	22	AA60414	Tomato seed expans
18	1026	81.5	227	17	AA694527	Cucumber expansin-
19	990	78.6	241	21	AA605452	Arabidopsis thalia
20	990	78.6	249	21	AA605451	Arabidopsis thalia
21	990	78.6	255	21	AA636570	Arabidopsis thalia
22	985	78.2	242	21	AA636569	Arabidopsis thalia
23	985	78.2	249	21	AA636568	Arabidopsis thalia
24	985	78.2	255	21	AA625443	Arabidopsis thalia
25	976.5	77.6	253	21	AA646483	Arabidopsis thalia
26	976.5	77.6	253	21	AA646482	Arabidopsis thalia
27	959.5	76.2	227	17	AA694532	Arabidopsis thalia
28	955	75.9	257	21	AA636445	Arabidopsis thalia
29	930.5	73.9	221	21	AA615694	Arabidopsis thalia
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31	930.5	73.9	255	21	AA651012	Arabidopsis thalia
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33	921	73.2	262	21	AA629930	Arabidopsis thalia
34	921	73.2	273	21	AA629930	Arabidopsis thalia
35	916	72.8	253	22	AA60412	Tomato seed expans
36	913	72.5	250	21	AA609622	Arabidopsis thalia
37	913	72.5	258	21	AA609621	Arabidopsis thalia
38	913	72.5	280	21	AA609620	Arabidopsis thalia
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41	898.5	71.4	222	17	AA694529	Rice expansin. Or
42	890.5	70.7	207	21	AA625444	Arabidopsis thalia
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44	859	68.2	225	17	AA694531	Arabidopsis expans
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ALIGNMENTS

RESULT 1	AA94528	standard; Protein; 228 AA.
XX	AA94528;	
AC	08-JUL-1996	(first entry)
XX		
DE	Rice expansin.	
XX	Expansin; plant cell wall; cellulose; paper recycling; de-inking;	
KW	polysaccharide; rice.	
XX		
OS	Oryza sativa.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 211	
FT		/note- "unidentified amino acid"
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PN	AA9540262-A.	
XX		
PD	04-APR-1996.	
XX		
PE	12-MAY-1994;	94AU-0068320.
XX		
PR	12-MAY-1995;	95US-0440517.
PR	12-MAY-1993;	93US-0060944.
XX		
PA	(PENN-) PENN STATE RES FOUND.	
XX		
PI	Cosgrove DJ, McQueen-Mason S;	
XX		
DR	WPI; 1996-201150/21.	
XX		


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? APPLICANT: McQueen-Watson, Simon
? APPLICANT: Gullitman, Mark J
? APPLICANT: Shcherban, Tatyana
? APPLICANT: Shi, Jun
? TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
? FILE REFERENCE: 1194/1C114US3
? CURRENT APPLICATION NUMBER: US/09/092.160C
? CURRENT FILING DATE: 1998-06-05
? EARLIER APPLICATION NUMBER: 08/440,517
? EARLIER FILING DATE: 1995-05-12
? EARLIER APPLICATION NUMBER: 08/242,090
? EARLIER FILING DATE: 1994-05-12
? EARLIER APPLICATION NUMBER: 08/060,944
? EARLIER FILING DATE: 1993-05-12
? NUMBER OF SEQ ID NOS: 7
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 4
? LENGTH: 227
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
? OTHER INFORMATION: expansin
? NAME/KEY: UNSURE
? LOCATION: (2)..(227)
? OTHER INFORMATION: Xaa is unknown or other.
? US-09-092-160-4

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QY 181 QMOSNLYNGQSLSFKYTTSDGQTVSNXNANAGWMSFGQFTGAHVR 228
DB 181 QMOSNLYNGQSLSFKYTTSDGQTVSNXNANAGWMSFGQFTGAHVR 228

RESULT 2

US-09-092-160-2

Sequence 2, Application US/09092160C
Patent No. 6255466

GENERAL INFORMATION:

APPLICANT: Cosgrove, Daniel J

APPLICANT: McQueen-Mason, Simon

APPLICANT: Gullitman, Mark J

APPLICANT: Shcherban, Tatyana

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

FILE REFERENCE: 1194/IC114053

CURRENT APPLICATION NUMBER: US/09/092,160C

EARLIER FILING DATE: 1998-06-05

EARLIER APPLICATION NUMBER: 08/440,517

EARLIER FILING DATE: 1995-05-12

EARLIER APPLICATION NUMBER: 08/242,090

EARLIER FILING DATE: 1994-05-12

EARLIER APPLICATION NUMBER: 08/060,944

EARLIER FILING DATE: 1993-05-12

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 228

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: rice expansin

FEATURE: NAME/KEY: UNSURE

LOCATION: 211

OTHER INFORMATION: Xaa is unknown or other.

US-09-092-160-2

Query Match 99.8%; Score 1257; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 6.5e-119;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 QMOSNLYNGQSLSFKYTTSDGQTVSNXNANAGWMSFGQFTGAHVR 228

RESULT 3

US-09-092-160-7

Sequence 7, Application US/09092160C
Patent No. 6255466

GENERAL INFORMATION:

APPLICANT: Cosgrove, Daniel J

APPLICANT: McQueen-Mason, Simon

APPLICANT: Gullitman, Mark J

APPLICANT: Shcherban, Tatyana

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

FILE REFERENCE: 1194/IC114053

CURRENT APPLICATION NUMBER: US/09/092,160C

EARLIER FILING DATE: 1998-06-05

EARLIER APPLICATION NUMBER: 08/440,517

EARLIER FILING DATE: 1995-05-12

EARLIER APPLICATION NUMBER: 08/242,090

EARLIER FILING DATE: 1994-05-12

EARLIER APPLICATION NUMBER: 08/060,944

EARLIER FILING DATE: 1993-05-12

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 227

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: cucumber

OTHER INFORMATION: expansin

US-09-092-160-7

Query Match 81.1%; Score 1021; DB 4; Length 227;
Best Local Similarity 78.8%; Pred. No. 3.7e-95;

Matches 175; Conservative 23; Mismatches 24; Indels 0; Gaps 0;

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DB 183 QMOSNLYNGQSLSFKYTTSDGQTVSNXNANAGWMSFGQFTGAHVR 224

RESULT 4

US-08-440-517A-6

Sequence 6, Application US/08440517A
Patent No. 5959082

GENERAL INFORMATION:

APPLICANT: COSGROVE, DANIEL J.

APPLICANT: GULLITMAN, MARK J.

APPLICANT: SCHERBAN, TATYANA;

APPLICANT: SHI, JUN

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE

ADDRESS: PENNSYLVANIA STATE UNIVERSITY

STREET: 113 TECHNOLOGY CENTER

CITY: UNIVERSITY PARK

STATE: PENNSYLVANIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 16802-7000

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: NEC 286

OPERATING SYSTEM: DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,517A

FILING DATE:

CLASSIFICATION: 530

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 226

TYPE: AMINO ACID

TOPOLOGY: UNKNOWN

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:54:05 ; Search time 8.91808 Seconds
(without alignments)
624.466 Million cell updates/sec

Title: US-09-896-301-2

Perfect score: 1259

Sequence: 1 AGCGWVAHAATFTGGGDSAG.....NNXANAGNSFGQTFGAHVR 228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1257	99.8	228	2	US-08-440-517A-2
2	1257	99.8	228	4	US-09-092-160-2
3	1021	81.1	227	4	US-09-092-160-7
4	959.5	76.2	226	2	US-08-440-517A-6
5	959.5	76.2	226	4	US-09-092-160-6
6	898.5	71.4	222	2	US-08-440-517A-3
7	898.5	71.4	222	4	US-09-092-160-3
8	859	68.2	225	2	US-08-440-517A-5
9	859	68.2	225	4	US-09-092-160-5
10	841	66.8	225	4	US-09-362-642-2
11	836	66.4	225	2	US-08-845-539-2
12	772	61.3	179	2	US-08-845-539-6
13	772	61.3	179	4	US-09-362-642-6
14	733.5	58.3	227	2	US-08-440-517A-4
15	733.5	58.3	227	4	US-09-092-160-4
16	711	56.5	167	2	US-08-845-539-4
17	711	56.5	167	4	US-09-362-642-4
18	731	18.3	261	1	US-07-971-096-2
19	231	18.3	261	1	US-08-175-096-2
20	222.5	17.7	246	4	US-08-441-507-21
21	220.5	17.5	272	4	US-08-441-507-15
22	212	16.8	263	1	US-07-971-096-4
23	212	16.8	263	1	US-08-175-096-4
24	212	16.8	263	4	US-08-413-974-6
25	212	16.8	263	4	US-08-434-418-6
26	212	16.8	263	4	US-08-433-288-6
27	212	16.8	263	4	US-08-174-739A-6

28	191.5	15.2	245	4	US-08-441-507-24	Sequence 24, Appl
29	154	12.2	197	4	US-08-441-507-5	Sequence 5, Appl
30	154	12.2	200	4	US-08-441-507-4	Sequence 4, Appl
31	152	12.1	122	4	US-08-441-507-23	Sequence 23, Appl
32	101	8.0	54	3	US-08-750-419A-12	Sequence 12, Appl
33	97.5	7.7	145	4	US-08-413-974-4	Sequence 4, Appl
34	97.5	7.7	145	4	US-08-434-418-4	Sequence 4, Appl
35	97.5	7.7	145	4	US-08-433-288-4	Sequence 4, Appl
36	97.5	7.7	145	4	US-08-174-739A-4	Sequence 4, Appl
37	83	6.6	1477	1	US-08-038-682-4	Sequence 4, Appl
38	83	6.6	1477	1	US-08-302-832-4	Sequence 4, Appl
39	83	6.6	1477	2	US-08-530-198-4	Sequence 4, Appl
40	83	6.6	1477	2	US-08-469-880-4	Sequence 4, Appl
41	83	6.6	1477	2	US-08-728-470-4	Sequence 4, Appl
42	83	6.6	1477	2	US-08-617-697-4	Sequence 4, Appl
43	83	6.6	1477	4	US-08-719-641-4	Sequence 4, Appl
44	82	6.5	1160	3	US-08-808-599A-24	Sequence 24, Appl
45	81	6.4	890	2	US-08-483-101-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-440-517A-2
; Sequence 2, Application US/08440517A
; Patent No. 5959082
; GENERAL INFORMATION:
; APPLICANT: COSGROVE, DANIEL J.;
; APPLICANT: GULLITMAN, MARK;
; APPLICANT: SCHERBAN, TATYANA;
; APPLICANT: SHI, JUN
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
; ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,517A
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
; US-08-440-517A-2
Query Match 99.8%; Score 1257; DB 2; Length 228;
Best local similarity 100.0%; Pred. No. 6.5e-119;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 AGCGWVAHAATFTGGGASGTMGACGYNLYSGYGTNTAALSTALFNNGLSCGACFEL 60
1 RCONDKGWCPCPSLVATATNFCPPNNALPNNAGGWCNPPQOHDLSQPVFORIAQYRAGI 120
61 RCONDKGWCPCPSLVATATNFCPPNNALPNNAGGWCNPPQOHDLSQPVFORIAQYRAGI 120
121 VPVAYRRVPCVRRGIRFTTNGHSYFNLVLTIVNGAGADVHSAMVKGSRGTGQAMSRNNG 180
121 VPVAYRRVPCVRRGIRFTTNGHSYFNLVLTIVNGAGADVHSAMVKGSRGTGQAMSRNNG 180

6

Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: AB4420; MUID:20083487

A:Accession: C84444

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-248 <STO>

A:Cross-references: GB:AE002093; NID:g3461833; PIDN:AC32927.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g03090

A:Map position: 2

C:Superfamily: expansin

Query Match 88.6%; Score 1115; DB 2; Length 248;

Best Local Similarity 87.1%; Pred. No. 2,3e-89;

Matches 196; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

4 GGNVNAHTFYGGSDASCTMGACGYGMLYSQGYCTNTAALSTALFNNGLSGACFEIRCO 63

24 GGNVNAHTFYGGSDASCTMGACGYGMLYSQGYCTNTAALSTALFNNGLSGACFEIRCO 83

64 NDGKWLPGSIVYATNFPCPPNNALPNNAGWCNPPQOHFDLSQPVFORIAQYRAGIYV 123

84 SDGAMCLPGALIVYATNFPCPPNNALPNNAGWCNPPRLHFDLSQPVFORIAQYRAGIYV 143

124 AYRRVPCVRKRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRGTGQAMSRNMGON 183

144 SYRRVPCMRKRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRGTGQAMSRNMGON 203

184 QSNSTYLNQGSLSFKYVTSDDQTVSNXNANAGSFGOTFTGAHV 228

204 QSNSTYLNQGSLSFKYVTSDDQTVSNXNANAGSFGOTFTGAHV 248

RESULT 3

T09821

expansin (clone ptepx3) - loblolly pine (fragment)

C:Species: Pinus taeda (loblolly pine)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000

C:Accession: T09821

R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.

A:Description: Expansins are conserved in conifers and expressed in response to exogenous

A:Reference number: 216866

A:Accession: T09821

A:Status: Preliminary; translated from GB/EMBL/DBDU

A:Molecule type: mRNA

A:Residues: 1-232 <HUT>

A:Cross-references: EMBL:U64891; NID:g1778100; PID:g1778101

A:Experimental source: clone ptepx3

C:Superfamily: expansin

Query Match 83.2%; Score 1047; DB 2; Length 232;

Best Local Similarity 79.1%; Pred. No. 1.7e-83;

Matches 178; Conservative 26; Mismatches 21; Indels 0; Gaps 0;

3 GGNVNAHTFYGGSDASCTMGACGYGMLYSQGYCTNTAALSTALFNNGLSGACFEIRCO 62

8 GGNVNAHTFYGGSDASCTMGACGYGMLYSQGYCTNTAALSTALFNNGLSGACFEIRCO 67

63 QNDGKWLPGSIVYATNFPCPPNNALPNNAGWCNPPQOHFDLSQPVFORIAQYRAGIYV 122

68 NDGPOMCLPGTYVYATNFPCPPNNALPNDNGWCNPPLOHFDMAEPALAKIYRAGIYV 127

123 VAYRRVPCVRKRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRGTGQAMSRNMGON 182

128 ILTYRVPCLRKRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRGTGQAMSRNMGON 187

183 WQSNSTYLNQGSLSFKYVTSDDQTVSNXNANAGSFGOTFTGAHV 227

188 WQSNSTYLNQGSLSFKYVTSDDQTVSNXNANAGSFGOTFTGAHV 232

RESULT 4

T09818

expansin (clone ptepx2) - loblolly pine (fragment)

C:Species: Pinus taeda (loblolly pine)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000

C:Accession: T09818

R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.

A:Description: Expansins are conserved in conifers and expressed in response to exoge

A:Reference number: 216866

A:Accession: T09818

A:Status: translated from GB/EMBL/DBDU

A:Molecule type: mRNA

A:Residues: 1-232 <HUT>

A:Cross-references: EMBL:U64890; NID:g1778098; PID:g1778099

A:Experimental source: clone ptepx2; hypocotyl

C:Superfamily: expansin

Query Match 82.8%; Score 1042; DB 2; Length 232;

Best Local Similarity 79.1%; Pred. No. 4.5e-83;

Matches 178; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

3 GGNVNAHTFYGGSDASCTMGACGYGMLYSQGYCTNTAALSTALFNNGLSGACFEIRCO 62

8 GGNVNAHTFYGGSDASCTMGACGYGMLYSQGYCTNTAALSTALFNNGLSGACFEIRCO 67

63 QNDGKWLPGSIVYATNFPCPPNNALPNNAGWCNPPQOHFDLSQPVFORIAQYRAGIYV 122

68 NDGPOMCLPGTYVYATNFPCPPNNALPNDNGWCNPPLOHFDMAEPALAKIYRAGIYV 127

123 VAYRRVPCVRKRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRGTGQAMSRNMGON 182

128 ILTYRVPCLRKRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRGTGQAMSRNMGON 187

183 WQSNSTYLNQGSLSFKYVTSDDQTVSNXNANAGSFGOTFTGAHV 227

188 WQSNSTYLNQGSLSFKYVTSDDQTVSNXNANAGSFGOTFTGAHV 232

RESULT 5

T09826

expansin (clone ptepx5) - loblolly pine (fragment)

C:Species: Pinus taeda (loblolly pine)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000

C:Accession: T09826

R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.

A:Description: Expansins are conserved in conifers and expressed in response to exoge

A:Reference number: 216866

A:Accession: T09826

A:Status: Preliminary; translated from GB/EMBL/DBDU

A:Molecule type: mRNA

A:Residues: 1-232 <HUT>

A:Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105

A:Experimental source: clone ptepx5

C:Superfamily: expansin

Query Match 83.3%; Score 1036; DB 2; Length 232;

Best Local Similarity 78.2%; Pred. No. 1.5e-82;

Matches 176; Conservative 28; Mismatches 21; Indels 0; Gaps 0;

3 GGNVNAHTFYGGSDASCTMGACGYGMLYSQGYCTNTAALSTALFNNGLSGACFEIRCO 62

8 GGNVNAHTFYGGSDASCTMGACGYGMLYSQGYCTNTAALSTALFNNGLSGACFEIRCO 67

63 QNDGKWLPGSIVYATNFPCPPNNALPNNAGWCNPPQOHFDLSQPVFORIAQYRAGIYV 122

68 NDGPOMCLPGTYVYATNFPCPPNNALPNDNGWCNPPLOHFDMAEPALAKIYRAGIYV 127

123 VAYRRVPCVRKRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRGTGQAMSRNMGON 182

128 ILTYRVPCLRKRGIRFTINGHSYFNLVLTINVGAGDVHSAMVKGSRGTGQAMSRNMGON 187

Genome version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:53:05 ; Search time 11.4421 Seconds
(without alignments)
1914.721 Million cell updates/sec

Title: US-09-896-301-2

Perfect score: 1259
Sequence: 1 AGGGMVNAHATFYGGDASG.....NNXANAGWSFGQFTGAHVR 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1246	99.0	237	2	T50654 expansin EXP1 [imp
2	1115	88.6	248	2	C84444 probable expansin
3	1047	83.2	232	2	T09821 expansin (clone pp
4	1042	82.8	232	2	T09818 expansin (clone pp
5	1036	82.3	232	2	T09826 expansin (clone pp
6	1028	81.7	232	2	T09825 expansin (clone pp
7	1026	81.5	250	2	T10079 expansin S1 precu
8	1001	79.5	246	2	T04175 expansin - rice
9	979	77.8	251	2	T03298 expansin 2 - rice
10	976.5	77.6	253	2	F84831 probable expansin
11	968	76.9	258	2	T09786 expansin - upland
12	955	75.9	257	2	D84820 probable expansin
13	936	74.3	257	2	T50658 expansin 9 [import
14	930.5	73.9	255	2	T50655 expansin EXP5 [imp
15	929	73.8	260	2	T47689 expansin-like prot
16	921	73.2	262	2	T02530 probable expansin
17	919.5	73.0	255	2	T50656 expansin EXP2 [imp
18	917	72.8	262	2	T50660 alpha-expansin 2 [
19	916	72.8	258	2	S53082 pollen allergen ho
20	913	72.5	258	2	T48247 expansin-like prot
21	910	72.3	261	2	T07630 alpha-expansin 1 -
22	910	72.3	264	2	T50659 expansin 1 - toma
23	908	72.1	257	2	T02727 probable expansin
24	908	72.1	259	2	T50653 expansin exp6 [imp
25	898	71.3	255	2	T06573 expansin 18 - toma
26	889	70.6	260	2	T10816 probable expansin
27	879	69.8	258	2	T10083 expansin S2 precu
28	863.5	68.6	261	2	T03737 expansin - rice
29	832.5	66.1	252	2	F86335 hypothetical prote

30	784	62.3	255	2	T02010 expansin homolog T
31	780.5	62.0	255	2	T03299 expansin 3 - rice
32	670	53.2	257	2	G96654 hypothetical prote
33	662	52.6	160	2	T09871 expansin - upland
34	662	52.6	257	2	F86259 protein T12C24.10
35	599	47.6	256	2	T05648 expansin homolog F
36	318.5	25.3	102	2	T09828 expansin (clone pp
37	302	24.0	77	2	T09815 expansin (clone pp
38	287	22.8	277	2	S48032 cimi protein - soy
39	282	22.4	276	2	T09041 cimi protein homol
40	274	21.8	81	2	T09830 expansin (clone pp
41	274	21.8	259	2	T50657 beta-expansin [imp
42	274	21.8	271	2	H84592 beta-expansin [imp
43	271	21.5	261	2	T04301 beta-expansin - ri
44	256.5	20.4	491	2	F96681 protein F1E22.6 [i
45	230.5	18.3	259	2	F84886 probable beta-expa

ALIGNMENTS

```

RESULT 1
T50654
expansin EXP1 [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C:Accession: T50654
R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shi
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A>Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
A:Reference number: Z14894; MUID:96016146
A:Accession: T50654
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-237 <SHC>
A:Cross-references: EMBL:U30476; PIDN:AA838070.1
A:Genetics:
A:Gene: EXP1
A:Function:
A:Description: induces extension (creep) in plant cell walls
C:Superfamily: expansin
C:Keywords: cell wall

Query Match          99.0%  Score 1246; DB 2; Length 237;
Best Local Similarity 98.7%; Pred. No. 9.4e-101;
Matches 225; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGGGMVNAHATFYGGDASGTMGACGYGNLYSGYGTNTALSTALFNNGISGACFEI 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 10 AGGGMVNAHATFYGGDASGTMGACGYGNLYSGYGTNTALSTALFNNGISGACFEI 69

OY 61 RCONDGKWCIPGSIYVYATNFCPPNNALPNNAGCMCPPOHFDLSQYFQRIAYRAGI 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 70 RCONDGKWCIPGSIYVYATNFCPPNNALPNNAGCMCPPOHFDLSQYFQRIAYRAGI 129

OY 121 VVAVARVPCVRGGRFTINGHSYFNVLITNVGAGDVHSAMKSGRTGQASRMWG 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 130 VVAVARVPCVRGGRFTINGHSYFNVLITNVGAGDVHSAMKSGRTGQASRMWG 189

OY 181 QMWQSNLYNGSLSEFKVTTSDQGTIVSNXNAGMSEFGQFTGAHVR 228
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 190 QMWQSNLYNGSLSEFKVTTSDQGTIVSNXNAGMSEFGQFTGAHVR 237

RESULT 2
C84444
probable expansin [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: C84444
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon,
eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

```


DB 221 GSGGALYSDDGIDDIDONAVYLFRFENALTTAIGKGAVC-----CLPTSGS 266
 QY 76 VFTATNCPNNALPNNAGCWCNPPQHPDISCPVFORIAQYRAGIYPVAVRRVPCVRCRG 135
 DB 267 STTV-----PIVTFSDKKQLVFERNNHSMKG--GAIYARRLSTSSGG 306
 QY 136 IRETINGHSYFNLVLTNNGA-----GPHSAMYKSGRTQWAMSRMGMQWQNSYL 189
 DB 307 PLTFINNISYAN---SQNLGGAIAIDTGGELISAKKGTIT-----FGGNRTSLPPL 355
 QY 190 NG-----QSLSF-KVTTSDQOTI 206
 DB 356 NGIHLDMNAKFKLKQARNGYSI 377

RESULT 14
 YMS5_CAEEL STANDARD; PRT; 1385 AA.

ID YMS5_CAEEL STANDARD; PRT; 1385 AA.
 AC P34501;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hypothetical 159.2 kDa protein K03H1.5 in chromosome III.
 GN K03H1.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Dunbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Lalister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden K.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K.,
 RA Watson R., Watson A., Weinstock L., Wilkinson-Sprat J.,
 RA Wohldman P.;
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).

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DR EMBL: Z29560; CAA82664.1; -;
 DR PIR: S41028; S41028.
 DR Wormpep: K03H1.5; CE03459.
 DR InterPro: IPR002909; IPT_TIG.
 DR InterPro: IPR003886; Nidogen_ext.
 DR InterPro: IPR000436; Nidogen_ext.
 DR InterPro: IPR001846; Vwd.
 DR Pfam: PF000884; sush1.1.
 DR Pfam: PF00094; vwd.2.
 DR SMART: SM00032; CCP.1.
 DR SMART: SM00429; IPT.1.
 DR SMART: SM00539; NIDO.1.
 DR SMART: SM00216; VMD.1.
 KW Hypothetical protein.
 SQ SEQUENCE 1385 AA; 159181 MW; BDCD8F59CEA38C03 CRC64;

Query Match 6.9%; Score 86.5; DB 1; Length 1385;
 Best Local Similarity 22.4%; Pred. No. 9.2;

Matches 50; Conservative 24; Mismatches 76; Indels 73; Gaps 10;
 QY 1 AGC-----GVNNAHAFYGGDASGTMG-GACGYGLYSOGYNTATLSTALFNNGISCG 55
 DB 393 AGGLDGFGGKQAMAGFNGNGCTGMYGLPYSGEGRMLKGY-----FSNVLP-- 439
 QY 56 ACEFIRQNDGW-----CLPGSI--VVTATNCPNNALPNNAGCWCNPE-- 99
 DB 440 -----PGWTHRVDEVIITPACTNANSGNMATAPWGPMDGMAINVSGLPLRAD 490
 QY 100 --QGHFDLSQVFORIAQYRAGIYPVAVRRVPCV-----RRCGIRETINGHSYFNLVLT 152
 DB 491 SVKVNFMNMTQTSRLSRVBARCIMPFMFKIGLIVIRMSRQGSFPPEKFFV----- 544
 QY 153 NVGAGDVHSAMVKG-----RTGQAMSRW 179
 DB 545 -VNSERAPASVSLKDSVDNKNRWYEPYAQELALGMAMNLTW 586

RESULT 15
 YF48_MYCTU STANDARD; PRT; 678 AA.

ID YF48_MYCTU STANDARD; PRT; 678 AA.
 AC Q10778;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical PPE-family protein RV1548C.
 GN RV1548C OR MT1599 OR MYCT48.17.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwim M.L., Haft D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ertolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -i SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.

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DR EMBL: Z74020; CAA98335.1; -;
 DR EMBL: AE007026; AAK45866.1; ALT_INIT.
 DR TIGR: MT1599; -;
 DR Tuberculist: RV1548C; -;
 DR InterPro: IPR002989; Mycobact_pentapep.

FT CHAIN 113 333 CATHEPSIN J.
 FT ACT_SITE 137 137 BY SIMILARITY.
 FT ACT_SITE 275 275 BY SIMILARITY.
 FT ACT_SITE 299 299 BY SIMILARITY.
 FT DISULFID 134 177 BY SIMILARITY.
 FT DISULFID 168 210 BY SIMILARITY.
 FT DISULFID 268 321 BY SIMILARITY.
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 42 42 P -> PK (IN REF. 2).
 SQ SEQUENCE 333 AA: 37147 MW: 7948FFID5A13B721 CRC64;

Query Match 7.4%; Score 93; DB 1; Length 333;
 Best Local Similarity 24.2%; Pred. No. 0.6;
 Matches 45; Conservative 15; Mismatches 72; Indels 54; Gaps 8;

QY 17 DASGTMGAGCGYGNLSQGYGTNTA--ALSTALFNNGLSGACF-----EIRCOND 65
 DB 167 DCSKTVG-----NKGQSGSTAHQAPEYVLKNGKLEAATPYEKGDPGRYASEN- 216
 QY 66 GKACGLGSIYVATNFCPPNNALPNNAGGCMPCQGHFDLSQPFQRIAYRAGIVPAY 125
 DB 217 -----ASANTIDYVNLPPNELYLVAVASIGFVSAIDASHDSFR----- 256
 QY 126 RRVPCVRGGIRFTINGHSYF--NLVLTINVGAGVHSAHYGSTRGQAMSRMGQNW 183
 DB 257 -----FYNGGITYEPNCSSTFVNHAVLVVGYGSEGD-----YADGNVYV-LINKSWGEEM 305
 QY 184 QSNSTL 189
 DB 306 GNMGYM 311

RESULT 11
 ROH2_HUMAN STANDARD; PRT: 449 AA.

AC P55795; O9HHA7;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Heterogeneous nuclear ribonucleoprotein H' (hnRNP H') (FMP-3).
 GN HNRPH2 OR FMP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95048329; PubMed=7959728;
 RA Vorechovsky I., Vetric D., Holland J., Bentley D.R., Thomas K.,
 RT Zhou J.N., Notarangelo L.D., Plebani A., Fontan G., Ochs H.D.;
 RT "Isolation of cosmid and cDNA clones in the region surrounding the
 RT BTK gene at Xq21.3-q22.";
 RT Genomics 21:517-524(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oeljen J.C., Liu X., Lu J., Malley T.M., Allen R.C., Muzny D.M.,
 RA Belmont J.W., Gibbs R.A.;
 RT Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=96081943; PubMed=7499401;
 RA Honore B., Rasmussen H.H., Vorum H., Dejgaard K., Liu X.,
 RA Gronov P., Madsen P., Gesser B., Tommerup N., Celis J.E.;
 RT "Heterogeneous nuclear ribonucleoproteins H', H', and F are members of
 RT a ubiquitously expressed subfamily of related but distinct proteins
 RT encoded by genes mapping to different chromosomes.";
 RT J. Biol. Chem. 270:28780-28789(1995).

CC -I- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENEOUS NUCLEAR
 CC RIBONUCLEOPROTEIN (HNRNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE
 CC FOR THE PROCESSING EVENTS THAT PRE-MRNAs UNDERGO BEFORE BECOMING

CC FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. BINDS POLY (RG).
 CC -I- SUBCELLULAR LOCATION: Nuclear; nucleoplasm.
 CC -I- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
 CC -I- SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
 CC -----
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 CC -----

DR EMBL: U01923; NOT ANNOTATED_CDS.
 DR EMBL: U78027; AAB64202.1; -.
 DR Aairus/Ghent-2DPAGE; 4432; IEF.
 DR MIM: 601036; -.
 DR InterPro: IPR000504; RRM.
 DR Pfam: PF00076; RRM; 3.
 DR SMART: SM00360; RRM; 3.
 DR PROSITE: PS00102; RRM; 3.
 DR PROSITE: PS00030; RRM_RNP_1; FALSE_NEG.
 KW Nuclear protein; RNA-binding; Ribonucleoprotein; Repeat.
 FT DOMAIN 11 90 RNA-BINDING (RRM) 1.
 FT DOMAIN 111 188 RNA-BINDING (RRM) 2.
 FT DOMAIN 289 364 RNA-BINDING (RRM) 3.
 FT REPEAT 234 433 2 X 16 AA GLY-RICH APPROXIMATE REPEATS.
 FT REPEAT 234 249 1-1.
 FT REPEAT 418 433 1-2.
 FT DOMAIN 354 392 2 X 19 AA PERFECT REPEATS.
 FT REPEAT 354 372 2-1.
 FT REPEAT 374 392 2-2.
 SQ SEQUENCE 449 AA: 49263 MW: C892523A638F07C7 CRC64;

Query Match 7.1%; Score 89; DB 1; Length 449;
 Best Local Similarity 20.3%; Pred. No. 1.8;
 Matches 48; Conservative 28; Mismatches 113; Indels 48; Gaps 8;

QY 2 GGGWNAHATPYGGDASGTMGAGCGYGNLSQGYGTNTALSTALFNNGLSGACFETR 61
 DB 225 GAGFERMRRAAGAGG-----YGGYDDYGG-YNDGYGFGSDRF-----GRDLNVCFS-- 269
 QY 62 CONDKWCLPGSIYVATNFCPPNNALPNNAG-----GMCNPPQGHFDL-----SQ 107
 DB 270 GMSDHRVGGSSPSTGHCYHMGRLPYRATENDITYFSPFLNPMRKHIEIGDGRVGT 329
 QY 108 PVFORIAYRAGIVPAYRVPCVRR-----GGIRFTINGHSYFNLVITNVCAG 158
 DB 330 EADVEFATHEDAVAMAKDKAMQHRVYELFLNSTAGTSGGAYDSYELFLNSTAGASG 389
 QY 159 DVHSAWVNGSR-----TGQAMSRNMGQNMNSYINGSLSKVITTSQGT 205
 DB 390 GAYGSGMMGMLGSLNOSYSGPASPQSLSGYGGYGGGSSMSGYDQVLQENSSDYQS 446

RESULT 12

YCC8_YEAST STANDARD; PRT: 405 AA.

AC P25367;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Hypothetical 42.6 kDa protein in Birk1-FUS1 intergenic region.
 GN YCLO28W OR YCLO28W OR YCLO181.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91377317; PubMed=1897318;
 RA Rad M.R., Luetzenkirchen K., Xu G., Kleinhaus U., Hollenberg C.P.;
 RT "The complete sequence of a 11,953 bp fragment from C1G on chromosome

Db 67 ASWCGAGCKCYOLTSTGQAPCSSCGTGAAGOSIIVMTNLCPN- -GNA-QWC--P 119
 QY 100 -----QOHPDL 105
 |||:
 Db 120 VVGSTNOGYGYVHDI 135

RESULT 9
 PER_DRONE STANDARD; PRT; 385 AA.
 AC P91686;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Period circadian protein (Fragment).
 GN PER.
 OS Drosophila nebulosa (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7271;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0761.0 PALMIRA / COLOMBIA;
 RX MEDLINE=97357421; PubMed=9214747;
 RA Gleason J.M., Powell J.R.;
 RT "Interspecific and intraspecific comparisons of the period locus in
 the Drosophila willistonii sibling species.";
 RL Mol. Biol. Evol. 14:741-753(1997).
 CC -1- FUNCTION: ESSENTIAL FOR BIOLOGICAL CLOCK FUNCTIONS. DETERMINES THE
 PERIOD LENGTH OF CIRCADIAN AND ULTRADIAN RHYTHMS; AN INCREASE IN
 PER DOSAGE LEADS TO SHORTENED CIRCADIAN RHYTHMS AND A DECREASE
 LEADS TO LENGTHENED CIRCADIAN RHYTHMS. ESSENTIAL FOR THE CIRCADIAN
 RHYTHMICITY OF LOCOMOTOR ACTIVITY, ECLOSION BEHAVIOR, AND FOR THE
 RHYTHMIC COMPONENT OF THE MALE COURTSHIP SONG THAT ORIGINATES IN
 THE THORACIC NERVOUS SYSTEM. THE BIOLOGICAL CYCLE DEPENDS ON THE
 RHYTHMIC FORMATION AND NUCLEAR LOCALIZATION OF THE TIM-PER
 COMPLEX. LIGHT INDICES THE DEGRADATION OF TIM, WHICH PROMOTES
 ELIMINATION OF PER. NUCLEAR ACTIVITY OF THE HETERODIMER
 COORDINATIVELY REGULATES PER AND TIM TRANSCRIPTION THROUGH A
 NEGATIVE FEEDBACK LOOP. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN
 TRANSCRIPTIONAL LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING
 INDIRECT TRANSCRIPTIONAL INHIBITION (BY SIMILARITY).
 CC -1- SUBUNIT: FORMS HETERODIMER WITH TIMELESS (TIM); THE COMPLEX THEN
 TRANSLOCATES INTO THE NUCLEUS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR AT SPECIFIC PERIODS OF THE DAY.
 CC FIRST ACCUMULATES IN THE PERINUCLEAR REGION ABOUT ONE HOUR BEFORE
 TRANSLOCATION INTO THE NUCLEUS. INTERACTION WITH TIM IS REQUIRED
 FOR NUCLEAR LOCALIZATION (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE
 DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLATION COULD BE IMPLICATED IN
 THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER
 PER-TIM (BY SIMILARITY).
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U51090; AAB41386.1; -
 DR FlyBase; FBgn0018750; DneVper.
 KW Biological rhythms; Repeat; Nuclear protein; Phosphorylation.
 FT NON_TER 1
 FT DOMAIN 102 112 POLY-GLY.
 FT DOMAIN 213 218 POLY-SER.
 FT DOMAIN 226 234 POLY-GLY.
 FT DOMAIN 246 252 POLY-GLY.
 FT DOMAIN 377 383 POLY-ALA.
 FT NON_TER 385 385
 SEQUENCE 385 AA; 39104 MW; A6C519E2CE66D5F0 CRC64;

Query Match 7.5%; Score 94.5; DB 1; Length 385;
 Best Local Similarity 26.3%; Pred. No. 0.52;
 Matches 41; Conservative 18; Mismatches 46; Indels 51; Gaps 9;

QY 1 AGGWNANATRYGGDASGTMGACGAGYGNLYSGYGTATLALSTALF-NGLSGCACE 59
 |||:
 Db 225 AGG-----GGGGGASGATCTGTGNGAGGGGGSNAOSTNMOYOSGLSC----- 269
 QY 60 IRCQNDGKN-----CLPGSIV-----VTATNFCPPNALDN-----NAGC 94
 |||:
 Db 270 --TQNTNLMPPSVGTTTPSVLSTHMAVAOSSFSPOHSLFPFTTYTPASTAASSPASCT 327
 |||:
 QY 95 WCNPF-PQOHPDL-----SQPVFORIAQYRAGIYPVAY 125
 |||:
 Db 328 SPNRPKHHTVHPSEOP---STSGAAMATMPLQY 360

RESULT 10
 CATL_MOUSE STANDARD; PRT; 333 AA.
 AC Q9R014; Q9WV51;
 ID CATL_MOUSE
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cathepsin J precursor (EC 3.4.22.-) (Cathepsin P) (CatLrp-P).
 GN CTSJ OR CTSJ.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=94556833; PubMed=10526153;
 RA Tislar K., Deussing J., Peters C.;
 RT "Cathepsin J, a novel murine cysteine protease of the papain family
 with a placenta-restricted expression.";
 RL FEBS Lett. 459:299-304(1999).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Placenta;
 RA Sol-Church K., French J., Troeber D., Mason R.W.;
 RT "Cloning of a mouse cysteine protease.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Lysosomal (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 PAPAIN FAMILY OF THIOL PROTEASES.
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 CC -----
 CC EMBL; AF136272; AAF13142.1; -
 DR EMBL; AF158182; AAD41898.1; -
 DR HSSP; P07711; 1CUL.
 DR MEROPS; C01.038; -
 DR MGD; MG1:1349426; Ctsj.
 DR InterPro; IPR000168; Peptidase_C1.
 DR InterPro; IPR000169; ThiolProt_act_site.
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR PRINTS; PR00705; PAPAIN.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
 DR Hydrolase; Thiol protease; Lysosome; Zymogen; Signal.
 FT SIGNAL 1 17
 FT PROPEP 18 112 ACTIVATION PEPTIDE.

RESULT 7

MP21_MAIZE STANDARD; PRT: 191 AA.

ID MP21_MAIZE

AC 007134;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Pollen allergen zea m 1 (Zea m 1).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Pollen;

RX MEDLINE=94010312; PubMed=8406014;

RA Broadwater A.H., Rubinstein A.L., Chay C.H., Klapper D.G., Redinger P.A.;

RT "Zea m1, the maize homolog of the allergen-encoding Lol pi gene of rye grass."

RL Gene 131:227-230(1993).

CC -1- TISSUE SPECIFICITY: POLLEN TISSUE.

CC -1- DEVELOPMENTAL STAGE: EXPRESSION LOW BEFORE AND HIGH AFTER POLLEN MITOSIS.

CC -1- DISEASE: CAUSES MAIZE POLLEN ALLERGY.

CC -1- SIMILARITY: BELONGS TO THE LOL P 1 FAMILY OF ALLERGENS.

CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.

CC -----

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CC -----

DR EMBL: L14271; AAA3496.1; -

DR PIR: JC1524; JC1524.

DR HSSP: P43214; IMHO.

DR MaizeDB: 65840; -

DR InterPro: IPR000882; Pollen.allergen.

DR Pfam: PF01357; Pollen.allergen.1.

DR PRINTS: PR01225; EXPANSINFAM1.

DR ProDom: PD002179; Pollen.allergen.1.

DR PROSITE: PS00843; EXPANSIN_CBD.1.

DR PROSITE: PS00842; EXPANSIN_EG45.1.

KW Allergen; Multigene family.

FT DOMAIN 1 91 EXPANSIN-LIKE EG45.

FT FT 105 186 EXPANSIN-LIKE CBD.

SQ SEQUENCE 191 AA; 21362 MW; 6E2A9DE921C45C63 CRC64;

Query Match 13.2%; Score 166; DB 1; Length 191;

Best local Similarity 24.5%; Pred. No. 2.2e-07;

Matches 49; Conservative 37; Mismatches 82; Indels 32; Gaps 8;

QY 40 TAAALSTALFNNGLSCGAFIRKONDGKWL--PGSIVTATNFCPPNNALPNNAGGCN 97

DB 2 TAGGNVPIFKDGKGCSCGEVRCRKEPE--CSGNPVTVFTIDMVEP----- 46

QY 98 PPOOHPLSPVFORIAQ-----YRAGIVPAVYRRVPCVRRGRIFFTINGHSYFN-- 147

DB 47 IAPVHPLLSKAGFSLKPLNDKLRLRHCIGIMDEFFRRVRCRKYPAQKIYHIEKGCNPNY 106

QY 148 -LVLTITVWGAGGVHSMVAGSRFG--WQAMSRNMGQWQMSN--YINGOSLSKVTTSOG 203

DB 107 VAVLVKFAVDGDIVLMEIODKLSAEKPKMLSMGAIWRMDTAKALG--PFSIRLTSESG 165

QY 204 QTIIVSNXANAGWSFGOTFT 223

DB 166 KKVIAKDIIPANWRPDAVYT 185

RESULT 8

GUN5_TKIRE STANDARD; PRT: 242 AA.

ID GUN5_TKIRE

AC P43317;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)

DE (Cellulase V) (EG V).

GN EGL5.

OS Trichoderma reesei (Hypocrea jecorina).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Hypocreaceae; Hypocrea.

OX NCBI_TaxID=51453;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=QM9414 / RUT C-30;

RX MEDLINE=95075308; PubMed=7984103;

RA Saloheimo A., Henttinen B., Hoffman A.-M., Telemann O., Penttilae M.;

RT "A novel, small endoglucanase gene, eg15, from Trichoderma reesei isolated by expression in yeast."

RL Mol. Microbiol. 13:219-228(1994).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose.

CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY K (FAMILY 45 OF GLYCOSYL HYDROLASES).

CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).

CC -----

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CC -----

DR EMBL: Z33381; CA83846.1; -

DR HSSP: P00725; 2CBH.

DR InterPro: IPR000254; CBD_fungal.

DR InterPro: IPR000334; Glyco_hydro_45.

DR Pfam: PF00734; CBD.1.1.

DR Pfam: PF02015; Glyco_hydro_45.1.

DR ProDom: PD001821; CBD_fungal.1.

DR SMART: SM00236; ICB1.

DR PROSITE: PS00562; CBD_FUNGAL.1.

DR PROSITE: PS00842; EXPANSIN_EG45.1.

DR PROSITE: PS01140; GLYCOSYL_HYDROL_F45.1.

KW Cellulose degradation; Hydrolase; Glycosidase; Signal.

FT SIGNAL 1 17

FT FT 18 242

FT CHAIN 18 242

FT ACT_SITE 27 27

FT ACT_SITE 134 134

FT DOMAIN 18 182

FT DOMAIN 183 205

FT DOMAIN 206 242

FT CARBOHYD 182 182

FT DISULFID 213 230

FT DISULFID 224 240

SQ SEQUENCE 242 AA; 24411 MW; CC033FC51326C71D CRC64;

Query Match 8.8%; Score 110.5; DB 1; Length 242;

Best local Similarity 30.9%; Pred. No. 0.014;

Matches 42; Conservative 12; Mismatches 35; Indels 47; Gaps 10;

QY 4 GWNAH-----ATFYGGGADSGTMGACGCGNLSXQ-----CYGTNTAALSTALFNN-- 50

DB 13 GAVSAYKATRTTRYYDQF-----GACGGGSSSGAFPMWLGIGNVYTAAGSQAFLFRAG 66

QY 51 -----GLSGACFEIR-----CONDGKWLPG-STIVTATNFCPPNNALPNNAGGCNPP 99

OS Phalaris aquatica (Canary grass).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Pooideae:
 OC Poaceae: Phalaris:
 OX NCBI_TaxID=28479;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pollen;
 RA MEDLINE=96105569; PubMed=8564724;
 RT Suphioglu C., Singh M.B.;
 RT "Cloning, sequencing and expression in Escherichia coli of pha 1
 RT and four isoforms of pha 5, the major allergens of canary grass
 RT pollen."
 RL Clin. Exp. Allergy 25:853-865(1995).
 RN [2]
 RP SEQUENCE OF 30-49.
 RX MEDLINE=93119091; PubMed=7687099;
 RA Suphioglu C., Singh M.B., Simpson R.J., Ward L., Knox R.B.;
 RT "Identification of canary grass (Phalaris aquatica) pollen allergens
 RT by immunoblotting: IgE and IgG antibody-binding studies."
 RL Allergy 48:273-281(1993).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
 CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: S80654; AAB35984.1; -.
 DR HSSP: P43214; IMHO.
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 DR PROSITE: PS50843; EXPANSIN_CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 DR Allergen: Glycoprotein; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 269 MAJOR POLLEN ALLERGEN PHA A 1.
 FT DOMAIN 67 173 EXPANSIN-LIKE EG45.
 FT DOMAIN 187 268 EXPANSIN-LIKE CBD.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 37 37 P -> G (IN REF. 2).
 FT CARBOHYD 37 37
 SQ SEQUENCE 269 AA; 05883A458ACE877F CRC64;
 Query Match 15.8%; Score 199; DB 1; Length 269;
 Best Local Similarity 26.8%; Pred. No. 4.8e-10;
 Matches 62; Conservative 39; Mismatches 100; Indels 30; Gaps 9;
 QY 2 GCGVWNAHATFVGGGDAAGT- -GAGCGYGNLYSQGYGTMTALSTALFNNGLSGCAFE 59
 D 44 GDKMLDAKSTYKPTGAGKPDNGAGCYKDYDKAPFNGMTCGNTPIFDGRCGSCFE 103
 QY 60 IRCONDKWCLPGSIYVYATNFCPPNNALPNNAGWCNPPQOHFDLSQPVFORIAQ- - 115
 D 104 LKSKRP- -ESCSEPTVITD- -DNEEP- -IAFYHEDLSGLAHFGSMKKGEE 150
 QY 116 - -YRAGIVPAVYRVPVRRGIRFTIN- -GHSYFNLVLTINVGAGDVHSAMK- G 167
 D 151 ENVRGAGLELEQFRRVKKYKPDGTRKPFHYEKGSPNPLVALLVYVGDGDVAVADIKK 210
 QY 168 SRTGQAMSRMNGMOSNS- -YINGOSLSFKVYTSQGITVSNNXNAGV 216
 D 211 GKDKWIELKESMGAIWRIDTPDKLTG- -PFTVRYTTGEGTKAFEDVYPRGV 260

RESULT 6
 ID MPOL_ORYSA
 AC 040638;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 01-MAR-2002 (rel. 41, Last annotation update)
 DE Major pollen allergen Ory s 1 precursor (Ory s 1).
 OS Oryza sativa (Rice).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae:
 OC Eriatoidae: Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=anther;
 RX MEDLINE=96069591; PubMed=7590339;
 RA Xu H., Theerakulpisut P., Goulding N., Suphioglu C., Singh M.B.,
 RA Bhalla P.L.;
 RT "Cloning, expression and immunological characterization of Ory s 1,
 RT the major allergen of rice pollen."
 RL Gene 164:255-259(1995).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MATURE ANTHERS BUT NOT IN
 CC VEGETATIVE OR OTHER FLORAL TISSUES.
 CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
 CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 CC -----
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 CC -----
 DR EMBL: U31771; AAA86533.1; -.
 DR HSSP: P43214; IMHO.
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 DR PROSITE: PS50843; EXPANSIN_CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 DR Allergen: Glycoprotein; Signal; Multigene family.
 FT SIGNAL 1 23
 FT CHAIN 24 263 MAJOR POLLEN ALLERGEN ORY S 1.
 FT DOMAIN 61 164 EXPANSIN-LIKE EG45.
 FT DOMAIN 178 259 EXPANSIN-LIKE CBD.
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 32 32
 SQ SEQUENCE 263 AA; 28497 MW; B1C5F24EA398DD60 CRC64;
 Query Match 13.4%; Score 168.5; DB 1; Length 263;
 Best Local Similarity 29.5%; Pred. No. 1.8e-07;
 Matches 57; Conservative 29; Mismatches 74; Indels 33; Gaps 11;
 QY 23 GAGCGYGNLYSQGY- -GTNTRALSTALFNNGLSGCAFEIRCONDKWC- -LGSIYVYVTR 79
 D 61 GACGKRYDDKAPFGLDMNSCG- -NDPIFKDGKCGSCFEIKSKRP- -EACSDKPLALHVTDM 118
 QY 80 NFCCPPNNALPNNAGWCNPPQOHFDLSQPVFORIAQ- -YRAGIVPAVYRVPVRRG 135
 D 119 NDPE- -IAFYHEDLSGLAHFGSMKKGEE- -WALKESMGAIWRIDTPK 164
 QY 136 IRFTIN- -GHSYFNLVLTINVGAGDVHSAMV- -KGSRTGQAMSRMNGMOSNS- - 187
 D 165 TKITFIEKASNNYVALLVYVGDGDVAVADIKKESGEE- -WKALKESMGAIWRIDTPK 223
 QY 188 YLNGOSLSFKVYTT 200
 D 224 PLKG-PPSVAVVT 235

RT group 1 allergens from eight different grass species." ;
 RL J. Allergy Clin. Immunol. 94:689-698(1994).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE LOI P I FAMILY OF ALLEGENS.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
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 CC
 DR EMBL: X78813; CA455390.1; -
 DR HSSP: P43214; IMHO.
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSIN_FAMLY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 DR PROSITE: PS50843; EXPANSIN_CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 KW Allergen; glycoprotein; Signal; Multigene family.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 1 263 POLLEN ALLERGEN PHL P 1.
 FT DOMAIN 61 167 EXPANSIN-LIKE EG45.
 FT DOMAIN 181 262 EXPANSIN-LIKE CBD.
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 263 AA; 28457 MW; 046BA249C17BC048 CRC64;
 Query Match 16.7%; Score 210; DB 1; Length 263;
 Best Local Similarity 27.3%; Pred. No. 5.5e-11;
 Matches 63; Conservative 40; Mismatches 98; Indels 30; Gaps 9;
 QY 2 GGGVNAHATFYGGDASGTM--GGACGYGNLYSGQYGTNTALSTALFNGLSCGACFE 59
 DB 38 GDEWLDASTWYKPTGAGKNDGACGYKDYDKPPFGMTGGGNPIFKSGRGSCSFE 97
 QY 60 IRCQNDGKWCLEPGSTIVTATNFCPPNNALPNNAGCNCPPQOHDLSQVFORIAQ--- 115
 DB 98 IKCTKP-EACSGEPVYVHTD---DNEP-----IAPYHFDLSGHAFGMAKKGDE 144
 QY 116 ---YRAGIVPAVYRRVPCVRGIRFTIN---GHSEYFNLYITNVGAGDVHSAWVK-G 167
 DB 145 QKRSAGLELDFRRKCKYPRBETKVTPEVEKSNPNYIALLVKYNGDGVVAVDIKER 204
 QY 168 SRTGQMSRMNGQMNQSN--YLNGQSLSPKVTSDGQTVSNXNAGW 216
 DB 205 GKDKMIELKESGAWVRIDTPDKLTG-PFYRYTTEGGTKTEADVIREGW 254
 RESULT 4
 MPAL_HOLLA STANDARD; PRT; 265 AA.
 ID MPAL_HOLLA 039975;
 AC P43216; G39975;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Major pollen allergen Hol 1 precursor (Hol 1 I) (Hol 1 I.0101 and
 DE 1.0102).
 OS Holcus lanatus (Velvet grass).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; Pooideae;
 OC Poaceae; Holcus.
 OC NCBI_TaxID=29679;
 RX Schramm G.D., Bufe A., Becker W.M., Schlaak M.;
 RX Schramm G.D., Bufe A., Becker W.M., Schlaak M.;
 RX Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE OF 18-265 FROM N.A.

RC STRAIN-CV. AVENEAE; TISSUE=Pollen;
 RX MEDLINE=97358126; Pubmed=9215246;
 RA Schramm G.D., Bufe A., Petersen A., Haas H., Schlaak M., Becker W.M.;
 RT "Mapping of IgE-binding epitopes on the recombinant major group 1
 RT allergen of velvet grass pollen, Hol 1 I." ;
 RL J. Allergy Clin. Immunol. 99:781-787(1997).
 RP [3]
 RP CHARACTERIZATION.
 RC STRAIN-CV. AVENEAE; TISSUE=Pollen;
 RX MEDLINE=96319506; Pubmed=8768603;
 RA Schramm G.D., Petersen A., Bufe A., Schlaak M., Becker W.M.;
 RT "Identification and characterization of the major allergens of velvet
 RT grass (Holcus lanatus), Hol 1 I and Hol 1 5." ;
 RL Int. Arch. Allergy Immunol. 110:354-363(1996).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE LOI P I FAMILY OF ALLEGENS.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
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 CC
 DR EMBL: Z27084; CA81610.1; -
 DR EMBL: Z68893; CA93121.1; -
 DR HSSP: P43214; IMHO.
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSIN_FAMLY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 DR PROSITE: PS50843; EXPANSIN_CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 KW Allergen; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 265 MAJOR POLLEN ALLERGEN HOL L 1.
 FT DOMAIN 63 169 EXPANSIN-LIKE EG45.
 FT DOMAIN 183 264 EXPANSIN-LIKE CBD.
 FT VARIANT 103 103 T -> S (IN HOL L 1.0102).
 SQ SEQUENCE 265 AA; 1FE23B3EE198AD6D CRC64;
 Query Match 15.8%; Score 199; DB 1; Length 265;
 Best Local Similarity 26.4%; Pred. No. 4.7e-10;
 Matches 61; Conservative 41; Mismatches 99; Indels 30; Gaps 9;
 QY 2 GGGVNAHATFYGGDASGTM--GGACGYGNLYSGQYGTNTALSTALFNGLSCGACFE 59
 DB 40 GDEWLDASTWYKPTGAGKNDGACGYKDYDKPPFGMTGGGNPIFKSGRGSCSFE 99
 QY 60 IRCQNDGKWCLEPGSTIVTATNFCPPNNALPNNAGCNCPPQOHDLSQVFORIAQ--- 115
 DB 100 IKCTKP-EACSGEPVYVHTD---DNEP-----IAPYHFDLSGHAFGMAKKGEE 146
 QY 116 ---YRAGIVPAVYRRVPCVRGIRFTIN---GHSEYFNLYITNVGAGDVHSAWVK-G 167
 DB 147 QKRSAGLELDFRRKCKYPRBETKVTPEVEKSNPNYIALLVKYNGDGVVAVDIKER 206
 QY 168 SRTGQMSRMNGQMNQSN--YLNGQSLSPKVTSDGQTVSNXNAGW 216
 DB 207 GKDKMIELKESGAWVRIDTPDKLTG-PFYRYTTEGGTKTEADVIREGW 256
 RESULT 5
 MPAL_PHAQA STANDARD; PRT; 269 AA.
 ID MPAL_PHAQA 041260;
 AC Q41260;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Major pollen allergen Pha a 1 precursor (Pha a 1).

Db 15 GSKWEAATATYEGSNPRGAAPDDHGGAGYKDVDKPEFDGMTACGNEPIFKDGLCCRACY 74

Qy 59 FIRCNDGCKWCLPGSIVVATATNFCEPNNALPNNMGCMCNPPQOHFDLSOPVQRTIAQ--- 115

Db 75 EIKCEPEVE-DSGEFVLKTTD-----KNYHIAAYHFDLSGKAFGAAGAKGQ 121

Qy 116 ---YRAGIVPVAVYRQVCVRGGRGIRFTIN---GHSYFNLLVLTNNVGAGDVHSAWKG 167

Db 122 EDKLKAKAGELTLPFRVACCKYPSGKRTFHEIKESNDHYLALLVYAAAGDGIYAVDIKP 181

Qy 168 SRTG-WQMSNRWGMQNO--SNSYINGCSLSKVTYTSQCQITVSNXNNAKSGFCQTF 223

Db 182 RDSEFIEMKSSWGAIWRIIDPKKPLKG-PFSIRLTSEGAHLVODVPIPAWKKPDVTYT 239

RESULT 2

MPIL_LOLPR STANDARD: PRT: 263 AA.

AC P14946; P14964; 01-APR-1990 (Rel. 14, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Lolium perenne (Perennial ryegrass).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Poaceae; Lolium.

OC Poaceae; Lolium.

OX NCBI_TaxID=4522;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90375479; Pubmed=1697854;

RA Perez M., Ishloka G.Y., Walker L.E., Chesnut R.W.;

RT "cDNA cloning and immunological characterization of the rye grass allergen Lol p I.";

RL J. Biol. Chem. 265:16210-16215(1990).

RN [2]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-48.

RC TISSUE=Pollen;

RX MEDLINE=91160716; Pubmed=2001733;

RA Griffith I.J., Smith P.M., Pollack J., Theerakulpisut P.,

RT Avjoughi A., Davies S., Hough T., Singh M.B., Simpson R.J., Ward L.D.,

RA Knox R.B.;

RT "Cloning and sequencing of Lol pI, the major allergenic protein of rye-grass pollen.";

RL FEBS Lett. 279:210-215(1991).

RN [3]

RP SEQUENCE OF 24-53.

RC TISSUE=Pollen;

RX MEDLINE=86242068; Pubmed=3718469;

RA Cottam G.P., Moran D.M., Standing R.;

RT "Physicochemical and immunochemical characterization of allergenic proteins from rye-grass (Lolium perenne) pollen prepared by a rapid and efficient purification method.";

RL Biochem. J. 234:305-310(1986).

RN [4]

RP SEQUENCE OF 236-263.

RX MEDLINE=89364850; Pubmed=2475768;

RA Esch R.E., Klapper D.G.;

RT "Isolation and characterization of a major cross-reactive grass group I allergenic determinant.";

RL Mol. Immunol. 26:557-561(1989).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- DISEASE: CAUSES GRASS POLLEN ALLERGY.

CC -1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.

CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE E645 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.

CC ---

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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:50:30 : Search time 5.8893 Seconds

(without alignments)
1499.000 Million cell updates/sec

Title: US-09-896-301-2

Perfect score: 1259

Sequence: 1 AGGWNVAHATFYGGDASG.....NNXANAGMSFGOTFGAHR 228

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SWISSPROT_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	214.5	17.0	246	1 MPCL_CYNDA	004701 cynodon dac
2	210	16.7	263	1 MPCL_LOLPR	P14946 lolium pere
3	210	16.7	263	1 MPPL_PHLPR	P43213 phleum prat
4	199	15.8	265	1 MPH1_HOLLA	P43216 holcus lana
5	199	15.8	269	1 MPAL_PHAAD	041260 phalaris ag
6	168.5	13.4	263	1 MPOL_ORISA	040638 oryza sativ
7	166	13.2	191	1 MP21_MAIZE	007154 zea mays (m
8	110.5	8.8	242	1 GUN5_TRIRE	P43317 trilochoderm
9	94.5	7.5	385	1 PER_DRONE	P91686 drosophila
10	93	7.4	333	1 CATJ_MOUSE	091014 mus musculu
11	89	7.1	449	1 ROH2_HUMAN	P55795 homo sapien
12	88.5	7.0	405	1 YCC8_YEAST	P25367 saccharomyc
13	86.5	6.9	922	1 PMPL_CHLPP	092995 chlamydia p
14	86.5	6.9	1385	1 YMS1_CAEEL	P34501 caenorhabdi
15	86	6.8	181	1 YF48_MYCTU	010778 mycobacteri
16	85	6.8	181	1 GUN1_MYTED	P82188 mytilus edu
17	84.5	6.7	207	1 EGG2_SCHJA	P19469 schistosoma
18	84.5	6.7	1429	1 LIT2_CAEEL	P14585 caenorhabdi
19	84	6.7	90	1 YV77_SNY3	P73455 synechocyst
20	84	6.7	1341	1 VG37_BPT2	P07667 bacteriophag
21	84	6.7	1656	1 OMPB_RICJA	006653 r outer mem
22	83	6.6	443	1 PORP_PSEAE	P32722 pseudomonas
23	81	6.4	223	1 VG32_BPMD2	064226 mycobacteri
24	80.5	6.4	677	1 SP87_DICDI	P54643 dictyostell
25	80.5	6.4	1403	1 YGN1_YEAST	P53127 saccharomyc
26	80	6.4	392	1 Y462_TREPA	O83475 treponema p
27	79.5	6.3	1300	1 L20K_RICRI	P14914 rickettsia
28	79.5	6.3	1654	1 OMPB_RICRI	053047 r outer mem
29	79	6.3	112	1 SEGC_HAEIN	P44713 haemophilus
30	79	6.3	212	1 EGG1_SCHJA	P19470 schistosoma
31	79	6.3	449	1 ROH1_HUMAN	P31943 homo sapien
32	79	6.3	465	1 GRP2_PPAVU	P10496 phaseolus v
33	79	6.3	751	1 VPA1_ROTGI	P15155 rotavirus (

34	78.5	6.2	391	1 PER_DRONE	P91613 drosophila
35	78.5	6.2	564	1 MERA_SHIFL	P08332 shigella fl
36	78.5	6.2	666	1 MUR2_ENTHR	P39046 enterococcu
37	78.5	6.2	1645	1 OMPB_RICRY	P66989 r outer mem
38	78	6.2	354	1 ALC_NEUCR	P18407 neurospora
39	78	6.2	378	1 ELYA_BACSP	P20724 bacillus sp
40	78	6.2	481	1 LORI_MOUSE	P18165 mus musculu
41	78	6.2	645	1 K22E_HUMAN	P35908 homo sapien
42	78	6.2	1246	1 YWV2_CAEEL	P34504 caenorhabdi
43	78	6.2	1964	1 NMC4_MOUSE	P31695 mus musculu
44	77.5	6.2	712	1 CPGT_BAC33	P09121 bacillus sp
45	77	6.1	571	1 FLA1_CAMEE	P56963 campylobact

ALIGNMENTS

RESULT 1	ID	MPCL_CYNDA	STANDARD:	PRT:	246 AA.
AC	004701:				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DE	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Major pollen allergen Cyn d 1.				
GN	CYNOL				
OS	Cynodon dactylon (Bermuda grass).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;				
OC	Chloridoideae; Cyndontae; Cynodon.				
OX	NCBI_TaxID=28909;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	TISSUE=Pollen.				
RX	MEDLINE=96347957; PubMed=8757211;				
RA	Smith P.M., Suphloglu C., Griffith I.J., Theriault K., Knox R.B.,				
RA	Singh M.B.;				
RT	*Cloning and expression in yeast Pichia pastoris of a biologically				
RT	active form of Cyn d 1, the major allergen of Bermuda grass pollen.;				
RL	J. Allergy Clin. Immunol. 98:331-343(1996).				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- DISEASE: CAUSES GRASS POLLEN ALLERGY.				
CC	-1- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLEGENS.				
CC	-1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.				
CC	-1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	or send an email to license@isb-sib.ch).				
DR	EMBL: S83343; AAB50734.2; -				
DR	HSSP: P43214; 1WHO.				
DR	InterPro: IPR000882: Pollen_allergen.				
DR	Pfam: PF01357: Pollen_allergen.1.				
DR	PRINTS: PR01225: EXPANSINFAMILY.				
DR	ProDom: PD002179: Pollen_allergen.1.				
DR	PROSITE: PS50843: EXPANSIN_CBD; 1.				
DR	PROSITE: PS50842: EXPANSIN_EG45; 1.				
KW	Allergen.				
FT	DOMAIN 39 145 EXPANSIN-LIKE EG45.				
FT	DOMAIN 159 240 EXPANSIN-LIKE CBD.				
FT	CARBOHYD 9 N-LINKED (GICNAC. . .) (POTENTIAL).				
SQ	SEQUENCE 246 AA: 26888 MW: 43D8442DBA588322 CRC64;				
QY	2 GGWNVAHATFYGG--GDASGTMGACGCGNLYSGYGTNTALSTALFNNGLSGACF 58				

Query Match Score 214.5; DB 1; Length 246;

Best Local Similarity 25.9%; Pred. No. 21e+11;

Matches 62; Conservative 44; Mismatches 102; Indels 31; Gaps 8;

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCB1_TaxID=3352;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=HYPOCOTYL;
 RA Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.;
 RT "Expansins are conserved in conifers and expressed in response to
 exogenous auxin."
 RL Submitted (Jul-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64890; AAA0634.1; ..
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMLY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 FT NON_TER 1
 SQ SEQUENCE 232 AA: 24734 MW: 1340AF483DE0741F CRC64:
 Query Match 82.8%; Score 1042; DB 10; Length 232;
 Best Local Similarity 79.1%; Pred. No. 5.2e-87;
 Matches 178; Conservative 25; Mismatches 22; Indels 0; Gaps 0;
 QY 3 GGVVNHATFYGGDASGTMGACGYGNLYSGYGTNTALSTALFNGLSCGACFEIRC 62
 DB 8 GGWESAHAATFYGGSDASGTMGACGYGNLYSGYGTNTALSTALFNGLSCGACYEMRC 67
 QY 63 QNDGKWCCLPGSIYVTAATNFCPPNNALPNNAGWCNPPQOHFDLSQPVFORIAQYRAGTVP 122
 DB 68 NDDPPQCLPFGTYVTAATNFCPPNNALPNDGWCNPPLOHFDPAEPALFLKAYRGITVP 127
 QY 123 VAVRRVPCVVRGSIREFTINGHSYFNLYLTNVGAGDVHSAMVKGSRGTGQAMSRNMGON 182
 DB 128 ILYTRVPCLRKGIREFTVNGHSYFNLYLTNVGAGDVHSAVSIKSGMSGMGQPMNRNMGON 187
 QY 183 WQSNSTLNGQSLSFEKVTTSDDGQTIYSNNXANAGWSFGQTFTGAHV 227
 DB 188 WQSNSTLNGQSLSFYVTTSDGRTIYSNNVAPSNWQFGQTFEGSQV 232

Search completed: October 11, 2002, 14:59:39
 Job time : 21.6871 secs

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ALPHA-EXPANSIN 3.
 OS Triphysaria versicolor.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusterids I; Lamiales; Orobanchaceae; Triphysaria.
 OX NCBI_TaxID=64093;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=ROOTS TREATED WITH DMBQ;
 RX MEDLINE=21186069; PubMed=11290422;
 RA Wrobel R.L., Yoder J.I.;
 RT "Differential RNA expression of alpha-expansin gene family members in
 the parasitic angiosperm *Triphysaria versicolor* (Scrophulariaceae).";
 RL Gene 266:85-93(2001).
 DR EMBL: AF230276; AAF32409.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PRO1225; EXPANSNFAMLY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 247 AA; 26456 MW; 0B2AC8F357CCE7B5 CRC64;
 Query Match 86.6%; Score 1090; DB 10; Length 247;
 Best Local Similarity 85.0%; Pred. No. 2,4e-91;
 Matches 192; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
 QY 3 GGVNNAHATFFGGDASGTMGACGCGNLYSOGYGTNTALSTALFNNGLSGACFEIRC 62
 DB 22 GGVNNAHATFFGGDASGTMGACGCGNLYSOGYGTNTALSTALFNNGLSGACFEIRC 81
 QY 63 QNDGKMCLEPGSIIVTATNFCPPNNALPNNAGGCMNPQOHFDLSQVFORIAQYRAGIVP 122
 DB 82 VNDGKMCLEPGSIIVTATNFCPPNNALPNNAGGCMNPRLHFDLADQVFGHIAQYRAGIVP 141
 QY 123 VAYRVPVCVRGGIRPTINGHSYFNLYLTNVGAGADVHSAMVKGSRGTGQMSRWGON 182
 DB 142 VAYRVPVCVRGGIRPTINGHSYFNLYLTNVGAGADVHSAMVKGSRGTGQMSRWGON 201
 QY 183 WQNSNLYNGOSLSFKYTTSDGQTIYSNNXNAGMSFGQFTGAHVR 228
 DB 202 WQNSNLYNGOSLSFKYTTSDGQTIYSNNXNAGMSFGQFTGAHVR 247
 RESULT 10
 Q9LBI PRELIMINARY: PRT; 242 AA.
 AC Q9LBI;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE EXPANSIN 3.
 OS Zinnia elegans.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusterids II; Asterales; Asteraceae; Asteroideae;
 OC NCBI_TaxID=34245;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20317189; PubMed=10859177;
 RA Im R.H., Cosgrove D.J., Jones A.M.;
 RT "Subcellular localization of expansin mRNA in xylem cells.";
 RL Plant Physiol. 123:463-470(2000).
 DR EMBL: AF230333; AAF35902.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen.1.
 DR PRINTS: PRO1225; EXPANSNFAMLY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 242 AA; 26157 MW; 168A0172AFCF5B58 CRC64;
 Query Match 83.5%; Score 1051.5; DB 10; Length 242;
 Best Local Similarity 83.5%; Pred. No. 7,5e-88;
 Matches 187; Conservative 15; Mismatches 17; Indels 5; Gaps 1;

QY 2 GGVNNAHATFFGGDASGTMGACGCGNLYSOGYGTNTALSTALFNNGLSGACFEIRC 61
 DB 21 GGVNNAHATFFGGDASGTMGACGCGNLYSOGYGTNTALSTALFNNGLSGACFEIRC 80
 QY 62 QNDGKMCLEPGSIIVTATNFCPPNNALPNNAGGCMNPQOHFDLSQVFORIAQYRAGIVP 121
 DB 81 QNDGKMCLEPGSIIVTATNFCPPNNALPNNAGGCMNPRLHFDLADQVFGHIAQYRAGIVP 135
 QY 122 VAYRVPVCVRGGIRPTINGHSYFNLYLTNVGAGADVHSAMVKGSRGTGQMSRWGON 181
 DB 136 VAYRVPVCVRGGIRPTINGHSYFNLYLTNVGAGADVHSAMVKGSRGTGQMSRWGON 195
 QY 182 WQNSNLYNGOSLSFKYTTSDGQTIYSNNXNAGMSFGQFTGA 225
 DB 196 WQNSNLYNGOSLSFKYTTSDGQTIYSNNXNAGMSFGQFTGA 239
 RESULT 11
 Q9FVG9 PRELIMINARY: PRT; 250 AA.
 AC Q9FVG9;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE EXPANSIN.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20532800; PubMed=11080302;
 RA Chen F., Bradford K.J.;
 RT "Expression of an Expansin Is Associated with Endosperm Weakening
 during Tomato Seed Germination.";
 RL Plant Physiol. 124:1265-1274(2000).
 DR EMBL: AF184233; AAG32921.1; -
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PRO1225; EXPANSNFAMLY.
 DR Prodom: PD002179; Pollen_allergen.1.
 SQ SEQUENCE 250 AA; 26821 MW; ADD1508763680CFD CRC64;
 Query Match 83.3%; Score 1049; DB 10; Length 250;
 Best Local Similarity 81.5%; Pred. No. 1,3e-87;
 Matches 181; Conservative 22; Mismatches 19; Indels 0; Gaps 0;
 QY 4 GGVNNAHATFFGGDASGTMGACGCGNLYSOGYGTNTALSTALFNNGLSGACFEIRC 63
 DB 26 GGVNNAHATFFGGDASGTMGACGCGNLYSOGYGTNTALSTALFNNGLSGACFEIRC 85
 QY 64 QNDGKMCLEPGSIIVTATNFCPPNNALPNNAGGCMNPQOHFDLSQVFORIAQYRAGIVP 123
 DB 86 QNDGKMCLEPGSIIVTATNFCPPNNALPNNAGGCMNPRLHFDLADQVFGHIAQYRAGIVP 145
 QY 124 VAYRVPVCVRGGIRPTINGHSYFNLYLTNVGAGADVHSAMVKGSRGTGQMSRWGON 183
 DB 146 VAYRVPVCVRGGIRPTINGHSYFNLYLTNVGAGADVHSAMVKGSRGTGQMSRWGON 205
 QY 184 QNSNLYNGOSLSFKYTTSDGQTIYSNNXNAGMSFGQFTGA 225
 DB 206 QNSNLYNGOSLSFKYTTSDGQTIYSNNXNAGMSFGQFTGA 247
 RESULT 12
 P93493 PRELIMINARY: PRT; 232 AA.
 AC P93493;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

RA Cronin L.A., Shen M., VanAken S.E., Unayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Selinger S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC004138; AAC32927.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMLY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 SQ SEQUENCE 248 AA: 26482 MW: 29E3199269B71271 CRC64;

Query Match 88.6%; Score 1115; DB 10; Length 248;
 Best Local Similarity 87.1%; Pred. No. 1.3e-93;
 Matches 196; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 4 GGWNAHATFFGGDASGTMGACGYNLVSOGYGTNTALSTALFNNGLSGACFEIRCO 63
 DB 24 GGWNAHATFFGGSDASGTMGACGYNLVSOGYGTNTALSTALFNNGLSGACFEIRCO 83
 QY 64 NDGKWLPGSIIVATATNFCPPNNALPNNAGGWCNPPQOHFDLSQPVFORIAQYRAGIVP 123
 DB 84 SDGKWLPGSIIVATATNFCPPNNALPNNAGGWCNPPQOHFDLSQPVFORIAQYRAGIVP 143
 QY 124 AYRRVPCVRRGIRFTTNGHSYFNLVLTNVGAGDVHSAMVKSGRTGQWMSRNMGCN 183
 DB 144 SYRRVPCVRRGIRFTTNGHSYFNLVLTNVGAGDVHSAMVKSGRTGQWMSRNMGCN 203
 QY 184 OSNSYLNQGSLSFKVTTSDGOTIVSNXNAGSFGOTFTGANVR 228
 DB 204 OSNNLNGQSLSEFKVTTSDGOTIVSNXNAGSFGOTFTGANVR 248

RESULT 7
 ID Q9M515 PRELIMINARY; PRT; 249 AA.
 AC Q9M515;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ALPHA-EXPANSIN 1;
 OS Tripharyxella versicolor;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusterids I; Lamiales; Orobanchaceae; Tripharyxella.
 NCBI_TaxID=64093;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ROOTS TREATED WITH DMBQ;
 RA MEDLINE-21186069; PubMed-11290422;
 RA Wrobel R.L., Yoder J.I.;
 RT "Differential RNA expression of alpha-expansin gene family members in
 the parasitic angiosperm Tripharyxella versicolor (Scrophulariaceae).";
 RL Gene 266:85-93(2001).
 DR EMBL: AF230278; AF232411.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR PRINTS: PR01225; EXPANSNFAMLY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 SQ SEQUENCE 249 AA: 26116 MW: DC976FEE376794FF CRC64;

Query Match 87.9%; Score 1106.5; DB 10; Length 249;
 Best Local Similarity 87.5%; Pred. No. 7.7e-93;
 Matches 196; Conservative 17; Mismatches 10; Indels 1; Gaps 1;
 QY 3 GGWNAHATFFGGDASGTMGACGYNLVSOGYGTNTALSTALFNNGLSGACFEIR 62
 ID Q9M517 PRELIMINARY; PRT; 247 AA.
 AC Q9M517;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)

DB 24 GGWNAHATFFGGDASGTMGACGYNLVSOGYGTNTALSTALFNNGLSGACFEIR 83
 QY 63 ONDGKWLPGSIIVATATNFCPPNNALPNNAGGWCNPPQOHFDLSQPVFORIAQYRAGIVP 122
 DB 84 VDDGKWLPGSIIVATATNFCPPNNALPNNAGGWCNPPQOHFDLSQPVFORIAQYRAGIVP 143
 QY 123 VAYRRVPCVRRGIRFTTNGHSYFNLVLTNVGAGDVHSAMVKSGRTGQWMSRNMGCN 182
 DB 144 VAYRRVPCVRRGIRFTTNGHSYFNLVLTNVGAGDVHSAMVKSGRTGQWMSRNMGCN 203
 QY 183 KOSNSYLNQGSLSFKVTTSDGOTIVSNXNAGSFGOTFTGANVR 225
 DB 204 KOSNNLNGQSLSEFKVTTSDGOTIVSNXNAGSFGOTFTGANVR 247

RESULT 8
 ID Q9P36 PRELIMINARY; PRT; 249 AA.
 AC Q9P36;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ALPHA-EXPANSIN PRECURSOR.
 GN NT-EXP4.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.
 NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. BY2;
 RA MEDLINE-99026292; PubMed-9808735;
 RA Link B.M., Cosgrove D.J.;
 RT "Acid-growth response and alpha-expansins in suspension cultures of
 bright yellow 2 tobacco";
 RL Plant Physiol. 118:907-916(1998).
 DR EMBL: AF049353; AAC96080.1; -;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSNFAMLY.
 DR ProDom: PD002179; Pollen_allergen; 1.
 KW Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 249 ALPHA-EXPANSIN.
 SQ SEQUENCE 249 AA: 26597 MW: 98F1D583B5E846CA CRC64;

Query Match 86.7%; Score 1092; DB 10; Length 249;
 Best Local Similarity 85.3%; Pred. No. 1.6e-91;
 Matches 191; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 2 GGWNAHATFFGGDASGTMGACGYNLVSOGYGTNTALSTALFNNGLSGACFEIR 61
 DB 23 GGWNAHATFFGGDASGTMGACGYNLVSOGYGTNTALSTALFNNGLSGACFEIR 82
 QY 62 CONDGKWLPGSIIVATATNFCPPNNALPNNAGGWCNPPQOHFDLSQPVFORIAQYRAGIV 121
 DB 83 CVDDRKGLPGSIIVATATNFCPPNNALPNNAGGWCNPPQOHFDLSQPVFORIAQYRAGIV 142
 QY 122 VAYRRVPCVRRGIRFTTNGHSYFNLVLTNVGAGDVHSAMVKSGRTGQWMSRNMGCN 181
 DB 143 VAYRRVPCVRRGIRFTTNGHSYFNLVLTNVGAGDVHSAMVKSGRTGQWMSRNMGCN 202
 QY 182 NMQNSYLNQGSLSFKVTTSDGOTIVSNXNAGSFGOTFTGANVR 225
 DB 203 NMQNNLNGQSLSEFKVTTSDGDRSLISYVAPRAHMSFGHTTGA 246

RESULT 9
 ID Q9M517 PRELIMINARY; PRT; 247 AA.
 AC Q9M517;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)

RC STRAIN=CV, COLUMBIA;
RA Durachko D.M., Sheherban T.Y., Cosgrove D.J.;
RT "Atxaplo is expressed in the trichomes, petioles, midribs, and pedicel
abscission zone."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006535; AAF87031.1; -
DR EMBL: AF229437; AAF61712.1; -
DR EMBL: AF229431; AAF61713.1; -
DR InterPro: IPR000882; Pollen_allergen.
DR PRINTS: PRO1225; EXPANSINFAMILY.
DR ProDom: PD002179; Pollen_allergen; 1.
SQ SEQUENCE 249 AA; 26428 MW; 63D014410DABBA1 CRC64;

Query Match 90.5%; Score 1139; DB 10; Length 249;
Best Local Similarity 89.0%; Pred. No. 8.6e-96;
Matches 202; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 2 GGGWNAHAATFYGGDASGTMGACGYGNLYSGYGTNTAALSTALFNNGLSGACFEIR 61
DB GGGWNAHAATFYGGDASGTMGACGYGNLYSGYGTNTAALSTALFNNGLSGACFEIR 82
QY 62 CONDKWCLPGSIVTATNFCPPNNALPNNAGCNCPPQOHEDLSQPVFORIAQYRAGIV 121
DB CENDGKWCLEPGSIVTATNFCPPNNALANNNGCNCPPLEHFDLAQPVFORIAQYRAGIV 142
QY 122 PVAYRRVPCVRRGIRFTINGHSYFNLVLTITNGAGADVHSANVKSRTGQWMSRNGQ 181
DB 143 PVAYRRVPCVRRGIRFTINGHSYFNLVLTITNGAGADVHSANVKSRTGQWMSRNGQ 202
QY 182 NMQNSYTLNGQSLSFKVTTSDDGQTIIVSNXNAGWSFCQTFGTGAHR 228
DB 203 NMQNSYTLNGQSLSFKVTTSDDGQTIIVSNXNAGWSFCQTFGTGAHR 249

RESULT 4

Q9FUM2 PRELIMINARY; PRT; 252 AA.
AC 09FUM2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EXPANSIN 2.
GN EXP2.
OS Prunus avium (Cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=42229;
RN 11
RP SEQUENCE FROM N.A.
RA Wu Z., Wiersma P.A.;
RT "Differential Expression of Expansin Genes Isolated from Sweet Cherry
(Prunus avium L.) During Fruit Ripening."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF297522; AAG13983.1; -
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PRO1225; EXPANSINFAMILY.
DR ProDom: PD002179; Pollen_allergen; 1.
SQ SEQUENCE 252 AA; 26766 MW; 5C62EBF83E5A138E CRC64;

Query Match 90.3%; Score 1137; DB 10; Length 252;
Best Local Similarity 89.0%; Pred. No. 1.3e-95;
Matches 202; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 2 GGGWNAHAATFYGGDASGTMGACGYGNLYSGYGTNTAALSTALFNNGLSGACFEIR 61
DB GGGWNAHAATFYGGDASGTMGACGYGNLYSGYGTNTAALSTALFNNGLSGACFEIR 85
QY 62 CONDKWCLPGSIVTATNFCPPNNALPNNAGCNCPPQOHEDLSQPVFORIAQYRAGIV 121
DB CENDGKWCLEPGSIVTATNFCPPNNALPNNAGCNCPPQOHEDLSQPVFORIAQYRAGIV 145

QY 122 PVAYRRVPCVRRGIRFTINGHSYFNLVLTITNGAGADVHSANVKSRTGQWMSRNGQ 181
DB 146 PVAYRRVPCVRRGIRFTINGHSYFNLVLTITNGAGADVHSANVKSRTGQWMSRNGQ 205
QY 182 NMQNSYTLNGQSLSFKVTTSDDGQTIIVSNXNAGWSFCQTFGTGAHR 228
DB 206 NMQNSYTLNGQSLSFKVTTSDDGQTIIVSNXNAGWSFCQTFGTGAHR 252

RESULT 5

Q93XP1 PRELIMINARY; PRT; 249 AA.
AC 093XP1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EXPANSIN.
GN EXP3.
OS Prunus cerasus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=140311;
RN 11
RP SEQUENCE FROM N.A.
RA Yoo S.-D., van Nocker S.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF350938; AAK48847.1; -
SQ SEQUENCE 249 AA; 26397 MW; C65556B038AB99D0 CRC64;

Query Match 89.0%; Score 1120; DB 10; Length 249;
Best Local Similarity 87.5%; Pred. No. 4.6e-94;
Matches 196; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGGGWNAHAATFYGGDASGTMGACGYGNLYSGYGTNTAALSTALFNNGLSGACFEI 60
DB SGGWNAHAATFYGGDASGTMGACGYGNLYSGYGTNTAALSTALFNNGLSGACFEI 82
QY 61 RCONDGKWCLEPGSIVTATNFCPPNNALPNNAGCNCPPQOHEDLSQPVFORIAQYRAGI 121
DB RCASDPKWWLPGLSIVTATNFCPPNNALPNNAGCNCPPQOHEDLSQPVFORIAQYRAGI 142
QY 121 PVAYRRVPCVRRGIRFTINGHSYFNLVLTITNGAGADVHSANVKSRTGQWMSRNGQ 180
DB 143 PVAYRRVPCVRRGIRFTINGHSYFNLVLTITNGAGADVHSANVKSRTGQWMSRNGQ 202
QY 181 NMQNSYTLNGQSLSFKVTTSDDGQTIIVSNXNAGWSFCQTFGTGAHR 224
DB 203 NMQNSYTLNGQSLSFKVTTSDDGQTIIVSNXNAGWSFCQTFGTGAHR 246

RESULT 6

080622 PRELIMINARY; PRT; 248 AA.
AC 080622;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE EXPANSIN.
GN AT2G03090.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN 11
RP SEQUENCE FROM N.A.

RC STRAIN=CV, COLUMBIA;
RA MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buehl C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Mofat K.S.,

QY 61 RCNDGKWCPLPGSIIVTATNCPNNALPNNAGWCNPPQHFDSLQVFORIAQYRAGI 120
 DB 70 RCNDGKWCPLPGSIIVTATNCPNNALPNNAGWCNPPQHFDSLQVFORIAQYRAGI 129
 QY 121 VPAVARRVPCVRRGCIIFTINGHSYFNLVLTNNVGAGDVHSAWVKSRTGQAMSRNWG 180
 DB 130 VPAVARRVPCVRRGCIIFTINGHSYFNLVLTNNVGAGDVHSAWVKSRTGQAMSRNWG 189
 QY 181 QNMOSNSYLNQSLSFVKYTTSDGQITVSNXNANAGMSFGQTFPGAHR 228
 DB 190 QNMOSNSYLNQSLSFVKYTTSDGQITVSNXNANAGMSFGQTFPGAHR 237

RESULT 2

Q9C554 PRELIMINARY: PRT: 250 AA.

ID Q9C554
 AC Q9C554
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE EXPANSIN PROTEIN (AT-EXP1).
 GN F10D13-18.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
 OC Eurosids II: Brassicales: Brassicaceae: Arabidopsis.
 OX NCBI_TaxID=3702;

NP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Tortum M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamuya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.
 RT "Full length cDNA of gene F10D13.18 (GI:12597783)."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

RC STRAIN=CV. COLUMBIA;
 RA MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Atafati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gull J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetelkale I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marzilli A.,
 RA Miltseher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana."
 RL Nature 408:816-820(2000).
 DR EMBL: AF360291; AAR6001.1; -;
 DR EMBL: AC073178; AAC60095.1; -;
 DR Interpro: IPR000882; Pollen_allergen.
 DR PRINTS: PR01225; EXPANSINFAML.
 DR PRODOM: PD002179; Pollen_allergen; 1.
 SO SEQUENCE 250 AA; 1D95EBA24FCE7E5 CRC64;

Query Match 99.0%; Score 1246; DB 10; Length 250;
 Best Local Similarity 98.7%; Pred. No. 1.6e-105;
 Matches 225; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 1 AGGGMVNAHATFYGGDASGTMGACGYNLYSGYGTNTAALSTALFNGLSCGACFEI 60

DB 23 AGGGMVNAHATFYGGDASGTMGACGYNLYSGYGTNTAALSTALFNGLSCGACFEI 82
 QY 61 RCNDGKWCPLPGSIIVTATNCPNNALPNNAGWCNPPQHFDSLQVFORIAQYRAGI 120
 DB 83 RCNDGKWCPLPGSIIVTATNCPNNALPNNAGWCNPPQHFDSLQVFORIAQYRAGI 142
 QY 121 VPAVARRVPCVRRGCIIFTINGHSYFNLVLTNNVGAGDVHSAWVKSRTGQAMSRNWG 180
 DB 143 VPAVARRVPCVRRGCIIFTINGHSYFNLVLTNNVGAGDVHSAWVKSRTGQAMSRNWG 202
 QY 181 QNMOSNSYLNQSLSFVKYTTSDGQITVSNXNANAGMSFGQTFPGAHR 228
 DB 203 QNMOSNSYLNQSLSFVKYTTSDGQITVSNXNANAGMSFGQTFPGAHR 250

RESULT 3

Q9LDR9 PRELIMINARY: PRT: 249 AA.

ID Q9LDR9
 AC Q9LDR9
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE T24P13.15 (EXPANSIN 10).
 GN EXP10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
 OC Eurosids II: Brassicales: Brassicaceae: Arabidopsis.
 OX NCBI_TaxID=3702;

NP SEQUENCE FROM N.A.
 RA Johnson-Hopson C., Dunn P., Brooks S., Buehler E., Chao Q., Khan S.,
 RA Kim C., Shinn P., Atafati H., Bel O., Chin C., Chou J., Choi E.,
 RA Conn L., Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Tortum M., Vaysberg M., Yu G., Federspiel N.A.,
 RA Theologis A., Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC T24P13 from chromosome
 1."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RC STRAIN=CV. COLUMBIA;
 RA Ecker J.R.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

NP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Atafati H., Bel B., Chin C., Chou J., Choi E.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howling B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Tortum M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RC STRAIN=CV. COLUMBIA;
 RA Cho H., Cosgrove D.J.;
 RT "Expansin ALEXPI0 affects organ growth and morphology in Arabidopsis
 thaliana."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: October 11, 2002, 14:51:00 ; Search time 19.6871 Seconds
(without alignments)
2003.488 Million cell updates/sec

Title: US-09-896-301-2

Perfect score: 1259
Sequence: 1 AGCGWVNAHATFYGGDASG.....NNXNAGWSFGQFTGAHVR 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioplasmid:*
17: sp_archaeoplasmid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1246	99.0	237	10	Q38863
2	1246	99.0	250	10	Q9C554
3	1139	90.5	249	10	Q9LDR9
4	1137	90.3	252	10	Q9FUM2
5	1120	89.0	249	10	Q93XP1
6	1115	88.6	248	10	Q80622
7	1106.5	87.9	249	10	Q9M515
8	1092	86.7	249	10	Q9M517
9	1090	86.6	247	10	Q9M517
10	1051.5	83.5	242	10	Q9LDR1
11	1049	83.3	250	10	Q9FVG9
12	1047	83.2	232	10	P93493
13	1047	83.2	253	10	Q9SWY1
14	1046	83.1	245	10	Q9LDR2
15	1042	82.8	232	10	P93492
16	1037	82.4	253	10	Q93XP2

17	1037	82.4	254	10	Q82093	082093 prunus arime
18	1037	82.4	260	10	Q9FNT0	Q9FNT0 cicer ariet
19	1036	82.3	232	10	P93495	P93495 pinus taeda
20	1034	82.1	254	10	Q9FUM3	Q9FUM3 prunus aviu
21	1029	81.7	249	10	Q9ZP35	Q9ZP35 nicotiana t
22	1028.5	81.7	252	10	Q9F530	Q9F530 prunus pers
23	1028	81.7	232	10	P93494	P93494 pinus taeda
24	1027	81.6	253	10	Q9SRT1	Q9SRT1 fragaria an
25	1026.5	81.5	252	10	Q81133	Q81133 prunus arime
26	1026	81.5	250	10	Q9ZP25	Q9ZP25 cucumis sat
27	1024	81.3	247	10	Q82625	Q82625 lycopersico
28	1020	81.0	276	10	Q94KT6	Q94KT6 zea mays (m
29	1010	80.2	239	10	Q9ZP31	Q9ZP31 lycopersico
30	1001	79.5	246	10	P93442	P93442 oryza sativ
31	1000	79.4	246	10	Q945J0	Q945J0 oryza sativ
32	996	79.1	291	10	Q9M4X8	Q9M4X8 oryza sativ
33	994	79.0	251	10	Q946J1	Q946J1 oryza sativ
34	993	78.9	253	10	Q94KT7	Q94KT7 zea mays (m
35	989	78.6	253	10	Q9SMD4	Q9SMD4 rumex palus
36	985	78.2	255	10	Q9FMA0	Q9FMA0 arabidopsis
37	979	77.8	251	10	Q40636	Q40636 oryza sativ
38	976.5	77.6	253	10	Q22874	Q22874 arabidopsis
39	973.5	77.3	245	10	Q9FNT1	Q9FNT1 cicer ariet
40	973	77.3	220	10	Q9AYR1	Q9AYR1 eustoma gra
41	968	76.9	258	10	Q49194	Q49194 gossypium h
42	955	75.9	257	10	Q48818	Q48818 arabidopsis
43	938	74.5	257	10	Q9SD24	Q9SD24 marsilea qu
44	936	74.3	257	10	Q9XG16	Q9XG16 lycopersico
45	931.5	74.0	252	10	Q9FY30	Q9FY30 festuca pra

ALIGNMENTS

RESULT 1
ID Q38863 PRELIMINARY: PRT: 237 AA.

AC Q38863: 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EXPANSIN AT-EXPI (FRAGMENT).
GN AT-EXPI.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucoisid II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016146; PubMed=7568110;
RA Shcherban T.Y., Shi J., Durachko D.M., Guiltinan M.J.,
RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansins--a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
DR EMBL: U30476; AAB38070.1; -
DR InterPro: IPR000882; Pollen_allergen.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS: PR01225; EXPANSINFAMILY.
DR PRODOM: PD002179; Pollen_allergen; 1.
FT NON_TER
SQ SEQUENCE 237 AA: 25155 MW; 0E5A2CB9C2943682 CRC64;

Query Match 99.0%; Score 1246; DB 10; Length 237;
Best local similarity 98.7%; Pred. No. 1.5e-105;
Matches 225; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCGWVNAHATFYGGDASGTGAGCGYGNLYSGYGTATLSTALFNNGLSCGACFEI 60
DB 10 AGCGWVNAHATFYGGDASGTGAGCGYGNLYSGYGTATLSTALFNNGLSCGACFEI 69